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124100

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Subject: seq. search in appl. no. 09/509,994

Please search all databases for the following sequences:

aa 19-516 of SEQ ID NO:1
aa 19-516 of SEQ ID NO:2

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Holly Schnizer
AU 1653
Office: REM 3C79
Mailbox: REM 3C70
(571)272-0958

CRIE

SUMMARY OF SEQ SRCH
PLEASE ~~keep~~ ^{SCAN} w/ SEARCH RESULTS

Searcher: _____
Phone: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 2
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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Lexis/Nexis: _____
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WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:39:53 ; Search time 53.5 Seconds
(without alignments)
2630.068 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516
Perfect score: 2830
Sequence: 1 APAEPQGGSCQVHDCFAL.....PSTPGSTLTPPAVLVHSG 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	100.0	498	AAR84185	Aar84185 Human der
2	2830	100.0	498	AAR01600	Aaw01600 Thrombomo
3	2830	100.0	516	AAR22016	Aar22016 Truncated
4	2830	100.0	516	AAY09347	Aay09347 Human thr
5	2830	100.0	516	AAY83934	Aay83934 Human thr
6	2830	100.0	516	AAY69529	Aay69529 Human thr
7	2830	100.0	516	ABU08701	Abu08701 Thrombomo
8	2830	100.0	516	ADA37271	Ada37271 Human sol
9	2830	100.0	575	AAR11534	Aar11534 Human thr
10	2830	100.0	575	AAR41806	Aar41806 Thrombomo
11	2830	100.0	575	AAR43031	Aar43031 Human thr
12	2830	100.0	575	AAR17521	Aae17521 Human ful
13	2830	100.0	575	AAR23026	Aae23026 Human thr
14	2827	99.9	557	AAR17528	Aae17528 Human thr
15	2827	99.9	557	AAR17525	Aae17525 Human thr
16	2827	99.9	557	AAR23031	Aae23031 Human thr
17	2827	99.9	557	AAR23028	Aae23028 Human thr
18	2826	99.9	516	AAR22018	Aar22018 Human thr
19	2826	99.9	516	AAY09348	Aay09348 Human thr
20	2826	99.9	516	AAY83935	Aay83935 Human thr
21	2826	99.9	516	ABU08703	Abu08703 Thrombomo
22	2826	99.9	516	ADA37275	Ada37275 Human sol
23	2826	99.9	557	AAR17523	Aae17523 Human thr
24	2826	99.9	575	ABG72575	Abg72575 Human thr
25	2826	99.9	575	ABM78950	Abm78950 Breast ca

26	2826	99.9	575	7	ADBS4760	Ade54760 Human Pro
27	2826	99.9	575	7	ADD48168	Add48168 Human Pro
28	2826	99.9	631	6	ABG72572	Abg72572 Human thr
29	2825	99.8	498	3	AAY67402	Aay67402 Novel sug
30	2825	99.8	557	5	AAR17596	Aae17596 Human thr
31	2824	99.8	497	2	AAW69520	Aaw69520 rstm prot
32	2824	99.8	557	5	AAE17530	Aae17530 Human thr
33	2824	99.8	557	5	AAE17598	Aae17598 Human thr
34	2823	99.8	557	5	AAE17526	Aae17526 Human thr
35	2823	99.8	557	5	AAE23029	Aae23029 Human thr
36	2822	99.7	516	2	AAR22017	Aar22017 Human thr
37	2822	99.7	557	5	AAE17593	Aae17593 Human thr
38	2822	99.7	557	5	AAE17595	Aae17595 Human thr
39	2822	99.7	557	5	AAE17597	Aae17597 Human thr
40	2822	99.7	557	5	AAE17529	Aae17529 Human thr
41	2822	99.7	557	5	AAE17527	Aae17527 Human thr
42	2822	99.7	557	5	AAE23030	Aae23030 Human thr
43	2821	99.7	557	5	AAE17592	Aae17592 Human thr
44	2821	99.7	557	5	AAE17594	Aae17594 Human thr
45	2821	99.7	557	5	AAE17591	Aae17591 Human thr

ALIGNMENTS

RESULT 1
AAR84185
ID AAR84185 standard; protein; 498 AA.
XX
AC AAR84185;
XX
DT 05-JUN-1996 (first entry)
XX
DE Human derived thrombomodulin.
XX
KW Human thrombomodulin; hepatopathy; fulminant hepatitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 349..463
FT /note= "fragment AAR84184"
XX
PN WO9528953-A1.
XX
PD 02-NOV-1995.
XX
PF 10-APR-1995; 95WO-JP000704.
XX
PR 20-APR-1994; 94JP-00081196.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
PI Fujiwara K, Mochida S;
XX
DR WPI; 1995-382844/49.
XX
PT Hepatopathy treatment pref. comprising human derived thrombomodulin -
XX
PS useful against, e.g, fulminant hepatitis.
XX
SQ Claim 2; Page 17-20; 29pp; Japanese.

Query Match 100.0%; Score 2830; DB 2: Length 498;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APAEPQGGSCQVHDCFALVPGPATFLNASQICDGLGHLMTVRSSVAADVISLLNGD 60
|||||

Db 1 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
 Qy 61 GGVGRRRLWIGLQPLPGCGDKRLGRLGFGOWTGDNNTSYSRWARLDLNGAPLCGLPLCV 120
 Db 61 GGVGRRRLWIGLQPLPGCGDKRLGRLGFGOWTGDNNTSYSRWARLDLNGAPLCGLPLCV 120
 Qy 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGMAAAVSIYGTGPPA 180
 Db 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGMAAAVSIYGTGPPA 180
 Qy 181 ARGADFOALPVGSSAAVAPLGLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Db 181 ARGADFOALPVGSSAAVAPLGLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Qy 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGVSCMCETGYRLAA 300
 Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGVSCMCETGYRLAA 300
 Qy 301 DOHRCEDVDDCILEPSPCQRCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Db 301 DOHRCEDVDDCILEPSPCQRCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Qy 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCECEPGYILDDGFI 420
 Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCECEPGYILDDGFI 420
 Qy 421 CTDIDECENGFGCGSVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGSEPPPS 480
 Db 421 CTDIDECENGFGCGSVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGSEPPPS 480
 Qy 481 PTPGSTLTTPPAVGLVHSG 498
 Db 481 PTPGSTLTTPPAVGLVHSG 498

RESULT 2

AAW01600
 ID AAW01600 standard; protein; 498 AA.

AC AAW01600;

DT 17-MAR-1997 (first entry)

DE Thrombomodulin TMB456 protein.

XX Thrombomodulin; nervous interference; treatment; medulla injury.

OS Homo sapiens.

PN JP08283174-A.

PD 29-OCT-1996.

PF 11-APR-1995; 95JP-00085202.

PR 11-APR-1995; 95JP-00085202.

PA (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1997-017314/02.

XX Treating agent for nervous interference after medulla injury - contains
 PT thrombomodulin as active component.

PS Claim 2; Page 5-6; 6pp; Japanese.

XX AAW01599-600 are fragments of human thrombomodulin. They can be used in
 CC treatment of nervous interference after medulla injury. In an example, a
 CC model of medulla injury was prepd. by compressing a male Wistar rat of
 CC 200-250 g body wt., with a 20g weight for 20 mins. TMD123 dissolved in
 CC physiological saline water was injected into the tail vein 30 mins.
 CC before injury. Movement function was evaluated 24 hrs. after injury. MPO
 CC activity in medulla tissue was measured 3 hrs. after injury as an index

CC of neutrophile accumulation. The Tarlov score was 1.50 compared to 0.77
 CC for the control, and complete paralysis was 15.4 percent compared to 35.3
 CC percent for the control
 XX SQ Sequence 498 AA;

Query Match 100.0%; Score 2830; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.1e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
 Db 1 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
 Qy 61 GGVGRRRLWIGLQPLPGCGDKRLGRLGFGOWTGDNNTSYSRWARLDLNGAPLCGLPLCV 120
 Db 61 GGVGRRRLWIGLQPLPGCGDKRLGRLGFGOWTGDNNTSYSRWARLDLNGAPLCGLPLCV 120
 Qy 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGMAAAVSIYGTGPPA 180
 Db 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGMAAAVSIYGTGPPA 180
 Qy 181 ARGADFOALPVGSSAAVAPLGLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Db 181 ARGADFOALPVGSSAAVAPLGLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Qy 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGVSCMCETGYRLAA 300
 Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGVSCMCETGYRLAA 300
 Qy 301 DOHRCEDVDDCILEPSPCQRCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Db 301 DOHRCEDVDDCILEPSPCQRCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Qy 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCECEPGYILDDGFI 420
 Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCECEPGYILDDGFI 420
 Qy 421 CTDIDECENGFGCGSVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGSEPPPS 480
 Db 421 CTDIDECENGFGCGSVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGSEPPPS 480
 Qy 481 PTPGSTLTTPPAVGLVHSG 498
 Db 481 PTPGSTLTTPPAVGLVHSG 498

RESULT 3

AAR22016
 ID AAR22016 standard; protein; 516 AA.

AC AAR22016;

XX 25-MAR-2003 (revised)

DT 03-JUL-1992 (first entry)

DE Truncated human thrombomodulin encoded by plasmid pSV2TMD1.

XX Thrombin binding site; blood clotting; TMD1 deleter.

OS Homo sapiens.

PN EP474273-A.

PD 11-MAR-1992.

XX 05-AUG-1991; 91EP-00202009.

PR 03-AUG-1990; 90JP-00204978.

PA (ASAH) ASAH KASEI KOGYO KK.

XX Zushi M, Gomi K, Yamamoto S, Suzuki K, Matsuda A;

XX DR WPI; 1992-081820/11.
 XX PT New polypeptide inhibits blood coagulation and platelet aggregation -
 XX PT promotes thrombin catalysed protein C activation for treating myocardial
 XX PT infarction, thrombosis, embolism, etc.
 XX PS Example 1; Page 17; 112pp; English.
 XX CC Plasmid M13mp19TMJ3 (see AAR22013) was used as template for site-directed
 CC mutagenesis. A 177bp fragment was deleted using the "TMD1 deleter"
 CC oligonucleotide to give plasmid M13TMD1 which encodes the first 516 N-
 CC terminal amino acids of human thrombomodulin. Plasmid M13TMD1 was
 CC completely digested with HindIII and BamHI and a TMD1 fragment of ca.
 CC 1700bp was isolated. The fragment was ligated to HindIII- and BglII-cut
 CC plasmid pSV2-dhfr to give the recombinant plasmid pSV2TMD1. See AAR22014-
 CC R22022 and AAR25072. (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 516 AA;

Query Match 100.0%; Score 2830; DB 2; Length 516;
 Best Local Similarity 100.0%; Pred. No. 1.1e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCVHEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCVHEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 78
 QY 61 GGVGRRRLWIGLQPPGCGDKPKRLGPGFOWVTGDNNTSYSRWRLDNGAPLCGLCV 120
 Db 79 GGVGRRRLWIGLQPPGCGDKPKRLGPGFOWVTGDNNTSYSRWRLDNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPIWEHQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSIYGTFFA 180
 Db 139 AVSAAEATVPSEPIWEHQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSIYGTFFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQGSYCMCETGYRLAA 300
 Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQGSYCMCETGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNVYDLVDGECVPEVDFCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNVYDLVDGECVPEVDFCFRANCEYQC 378
 QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNOTACPADCPNTQASCECEGYLLDDGFI 420
 Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNOTACPADCPNTQASCECEGYLLDDGFI 438
 QY 421 CTDIDCEGCGFSGVCHNLPGTFECICGPDLSALVRHIGTDCSGKVDGSDSGSGEPSPS 480
 Db 439 CTDIDCEGCGFSGVCHNLPGTFECICGPDLSALVRHIGTDCSGKVDGSDSGSGEPSPS 498
 QY 481 PTPGSTLTTPPAVLVHSG 498
 Db 499 PTPGSTLTTPPAVLVHSG 516

RESULT 4
 AAY09347
 ID AAY09347 standard; protein; 516 AA.
 AC AAY09347;
 XX AAY09347;
 XX 08-JUL-1999 (first entry)
 XX Human thrombomodulin SEQ ID NO:1.
 XX Human; thrombomodulin; aqueous parenteral solution; storage;
 KW distribution; acute coronary syndrome; thrombosis; embolism; diabetes.

XX OS Homo sapiens.
 XX PN WO9918994-A1.
 XX XX 22-APR-1999.
 XX XX 13-OCT-1998; 98WO-JP004609.
 XX PR 15-OCT-1997; 97JP-00281659.
 XX PR 11-NOV-1997; 97JP-00308523.
 XX PA (ASAH) ASAH KASEI KOGYO KK.
 XX PI Yui M, Yokozawa A, Murata T, Tsuruta K, Shimizu H;
 XX WPI; 1999-277444/23.
 XX DR N-ESDB; AAX55879.

Stable aqueous parenteral thrombomodulin solution - comprising buffer and surfactant, useful for treating acute coronary syndrome, thrombosis, embolism, and diabetes.

Claim 6; Page 87-89; 97pp; Japanese.

The present invention describes a method for maintaining the quality of an aqueous parenteral solution of thrombomodulin comprising buffer and surfactant aseptically filled in a case or syringe. Maintaining the quality of an aqueous, parenteral thrombomodulin solution is characterised in that the solution: (a) comprises soluble thrombomodulin, a buffer to maintain the pH at 5-7 and a surfactant; (b) is aseptically filled into: (i) a case or (ii) a syringe without any empty space; and (c) is kept in liquid form in storage and distribution and not frozen or freeze dried. Thrombomodulin is used to treat acute coronary syndrome (such as myocardial infarction, unstable angina and coronary artery blockage), thrombosis (e.g. cerebral, vascular and peripheral blood vessel thrombosis), embolism, peripheral blood vessel disorders (e.g. Raynaud's disease), arteriosclerosis, vasculitis (e.g. due to systemic lupus erythematosus or Barret's syndrome), multiple organ failure, disseminated intravascular coagulation, transient ischaemia, diabetes, liver veno-occlusive diseases and deep vein thrombosis. The composition is stable for a long period of time and can be stored and distributed in ready to use form avoiding the problems of dissolution and accuracy when preparing on demand. The present sequence represents human thrombomodulin

SQ Sequence 516 AA;

Query Match 100.0%; Score 2830; DB 2; Length 516;
 Best Local Similarity 100.0%; Pred. No. 1.1e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCVHEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCVHEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 78
 QY 61 GGVGRRRLWIGLQPPGCGDKPKRLGPGFOWVTGDNNTSYSRWRLDNGAPLCGLCV 120
 Db 79 GGVGRRRLWIGLQPPGCGDKPKRLGPGFOWVTGDNNTSYSRWRLDNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPIWEHQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSIYGTFFA 180
 Db 139 AVSAAEATVPSEPIWEHQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSIYGTFFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQGSYCMCETGYRLAA 300
 Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQGSYCMCETGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNVYDLVDGECVPEVDFCFRANCEYQC 360

Db 319 DQRCEDVDDCILEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPCFRANCEYQC 378

QY 361 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCQACPADCDPNTQASCCEPGYILDDGFI 420

Db 379 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCQACPADCDPNTQASCCEPGYILDDGFI 438

QY 421 CTIDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDCKVDDGSGSGGEPPEPS 480

Db 439 CTIDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDCKVDDGSGSGGEPPEPS 498

QY 481 PTPGSTLTTPPAVGLVHSG 498

Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 5

AAV83934

ID AAY83934 standard; protein; 516 AA.

XX AC AAY83934;

DT 28-JUL-2000 (first entry)

DE Human thrombomodulin TMD protein.

XX Human; thrombomodulin; vasculitis; protein C; thrombin.

KW Homo sapiens.

XX OS

XX JP2000053582-A.

XX 22-FEB-2000.

XX 06-AUG-1998; 98JP-00222688.

XX 06-AUG-1998; 98JP-00222688.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 2000-353249/31.

XX N-PSDB; AAA10027.

XX Treating agent for vasculitis contains peptide which promotes activation

PT of proterin C by thrombin.

XX Claim 4; Page 10-12; 18pp; Japanese.

XX This sequence represents a human thrombomodulin protein. The invention

CC relates to a treating agent for vasculitis containing a peptide which

CC promotes activation of protein C by thrombin

XX Sequence 516 AA;

QY Query Match 100.0%; Score 2830; DB 3; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.1e-149;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAADVLSLLNGD 60

Db 19 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAADVLSLLNGD 78

QY 61 GGVRRRLWIGLQIPGCGDPPKRLGPIRGQWVTGDNNTSYSRWRLDLNGAPLQGPLCV 120

Db 79 GGVRRRLWIGLQIPGCGDPPKRLGPIRGQWVTGDNNTSYSRWRLDLNGAPLQGPLCV 138

QY 121 AVSAAEATVSEPIWEQQCEVKGADGFLCFRHPFATCRPLAVEPFGAAAAVSYTYGTPFA 180

Db 139 AVSAAEATVSEPIWEQQCEVKGADGFLCFRHPFATCRPLAVEPFGAAAAVSYTYGTPFA 198

QY 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240

Db 199 ARGADFQALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 258

QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300

Db 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318

QY 301 DOHRCEDVDDCILEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPCFRANCEYQC 360

Db 319 DOHRCEDVDDCILEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPCFRANCEYQC 378

QY 361 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCQACPADCDPNTQASCCEPGYILDDGFI 420

Db 379 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCQACPADCDPNTQASCCEPGYILDDGFI 438

QY 421 CTIDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDCKVDDGSGSGGEPPEPS 480

Db 439 CTIDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDCKVDDGSGSGGEPPEPS 498

QY 481 PTPGSTLTTPPAVGLVHSG 498

Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 6

AAV69529

ID AAY69529 standard; protein; 516 AA.

XX AC AAY69529;

DT 10-APR-2000 (first entry)

DE Human thrombomodulin variant, SEQ ID NO:3.

XX Thrombomodulin; TM; soluble; affinity purification; cation exchange;

KW anticoagulant; thrombolytic.

XX OS Homo sapiens.

XX JP113411990-A.

XX 14-DEC-1999.

XX 23-MAR-1999; 99JP-00077518.

XX 30-MAR-1998; 98JP-00084389.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 2000-101696/09.

XX N-PSDB; AAZ55965.

XX Preparation of highly pure soluble thrombomodulin - used as an antibody

PT coagulation agent and a thrombolytic agent.

XX Claim 9; Page 30-32; 36pp; Japanese.

XX The invention relates to a novel method for the preparation of highly

CC pure soluble thrombomodulin (TM) containing substantially no serum-

CC derived or antibody-derived substance. The method comprises isolating

CC soluble TM from unpurified serum via affinity purification using an anti-

CC TM antibody. The soluble TM is then treated with a cation exchanger

CC at a specific conductivity of 25 to 34 ms/cm and a pH of 3 to 4, and the

CC fraction containing the soluble TM is isolated. The soluble TM can be

CC used as a blood anticoagulation agent and a thrombolytic agent. This

CC sequence represents a human thrombomodulin variant, designated SEQ ID

CC NO:3

XX Sequence 516 AA;

QY Query Match 100.0%; Score 2830; DB 3; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.1e-149;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAADVLSLLNGD 60

Db 19 APAEPQGGSCVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSILLNGD 78
 Qy 61 GVGRRRLWIGLQPPGGDKRGLPGRFQWVTGDNNTSYSRWARLDNGAPLCGPLCV 120
 Db 79 GVGRRRLWIGLQPPGGDKRGLPGRFQWVTGDNNTSYSRWARLDNGAPLCGPLCV 138
 Qy 121 AVSAAEATVPSEPIWEEQOCEVKADGFLCEHFHFPATCRPLAVEPGAAAAAASITYGTFFA 180
 Db 139 AVSAAEATVPSEPIWEEQOCEVKADGFLCEHFHFPATCRPLAVEPGAAAAAASITYGTFFA 198
 Qy 181 ARGADFQALFVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
 Db 199 ARGADFQALFVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 258
 Qy 241 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSVCMTGYRLAA 300
 Db 259 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSVCMTGYRLAA 318
 Qy 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHECHYPNYDLVDGECVEPYDPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHECHYPNYDLVDGECVEPYDPCFRANCEYQC 378
 Qy 361 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYILDDGFI 420
 Db 379 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYILDDGFI 438
 Qy 421 CTIDECENGFCGSGVCHNLPGTEFCICGPDSSALVRHIGTDCDVGKVDGSGSGGEPPTS 480
 Db 439 CTIDECENGFCGSGVCHNLPGTEFCICGPDSSALVRHIGTDCDVGKVDGSGSGGEPPTS 498
 Qy 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 7

ABU08701
 ID ABU08701 standard; protein; 516 AA.
 AC ABU08701;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Thrombomodulin-containing composition associated protein #1.
 XX
 KW Thrombomodulin; antiplatelet; anticoagulant; thrombolytic;
 KW blood coagulation-fibrinolysis system; vascular obstruction;
 KW myocardial infarction; acute coronary syndrome; brain infarction; sepsis;
 KW cardiact; cerebroprotective; antibacterial; immunosuppressive;
 KW anticoagulant; thrombolytic.
 XX
 OS Unidentified.
 XX
 PN WO2003013606-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 07-AUG-2002; 2002WO-JP008058.
 XX
 PR 08-AUG-2001; 2001JP-00241371.
 XX
 PA (ASAH) ASAHI KASEI KOGYO KK.
 XX
 PI Suzuki H, Mohri M;
 XX
 DR WPI; 2003-248241/24.
 DR N-PSDB; ABX94087.
 XX
 PT Thrombomodulin-containing medicinal compositions useful for treating or
 PT preventing e.g. myocardial infarction, brain infarction, acute coronary
 XX syndrome and sepsis.
 PS Claim 18; Page 29-31; 48pp; Japanese.

XX
 CC The invention describes drug compositions containing thrombomodulin, and
 CC an antiplatelet, an anticoagulant or/ and a thrombolytic other than
 CC thrombomodulin. The drug compositions are for preventing or treating
 CC diseases or syndromes due to abnormality in the blood coagulation-
 CC fibrinolysis system or/and vascular obstruction, including myocardial
 CC infarction, acute coronary syndrome, brain infarction and sepsis,
 CC particularly as combination drug compositions. The compositions have high
 CC therapeutic efficacy. This is the amino acid sequence of a thrombomodulin
 CC -containing composition associated protein
 XX
 SQ Sequence 516 AA;

Query Match 100.0%; Score 2830; DB 6; Length 516;
 Best Local Similarity 100.0%; Pred. No. 1.1e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 APAEPQGGSCVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSILLNGD 60
 Db 19 APAEPQGGSCVHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSILLNGD 78
 Qy 61 GVGRRRLWIGLQPPGGDKRGLPGRFQWVTGDNNTSYSRWARLDNGAPLCGPLCV 120
 Db 79 GVGRRRLWIGLQPPGGDKRGLPGRFQWVTGDNNTSYSRWARLDNGAPLCGPLCV 138
 Qy 121 AVSAAEATVPSEPIWEEQOCEVKADGFLCEHFHFPATCRPLAVEPGAAAAAASITYGTFFA 180
 Db 139 AVSAAEATVPSEPIWEEQOCEVKADGFLCEHFHFPATCRPLAVEPGAAAAAASITYGTFFA 198
 Qy 181 ARGADFQALFVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
 Db 199 ARGADFQALFVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 258
 Qy 241 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSVCMTGYRLAA 300
 Db 259 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSVCMTGYRLAA 318
 Qy 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHECHYPNYDLVDGECVEPYDPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHECHYPNYDLVDGECVEPYDPCFRANCEYQC 378
 Qy 361 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYILDDGFI 420
 Db 379 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYILDDGFI 438
 Qy 421 CTIDECENGFCGSGVCHNLPGTEFCICGPDSSALVRHIGTDCDVGKVDGSGSGGEPPTS 480
 Db 439 CTIDECENGFCGSGVCHNLPGTEFCICGPDSSALVRHIGTDCDVGKVDGSGSGGEPPTS 498
 Qy 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 8

ADA37271
 ID ADA37271 standard; protein; 516 AA.
 AC ADA37271;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human soluble thrombomodulin protein SEQ ID NO:1.
 XX
 KW high-concentration preparation; soluble thrombomodulin; human;
 KW thrombomodulin.
 XX
 OS Homo sapiens.
 XX
 PN WO2003061687-A1.
 XX
 PD 31-JUL-2003.
 XX

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PF 17-JAN-2003; 2003WO-JF000339.
XX
PR 18-JAN-2002; 2002JP-00009951.
XX
PA (ASAH ) ASahi KASEI KK.
XX
PI Nishio F;
XX
DR WPI; 2003-712487/67.
XX
DR N-PSDB; ADA37272.
XX
PT High concentration stable low-foaming soluble thrombomodulin preparation
PT for pharmaceutical use.
XX
XX Claim 18; Page 96-98; 113pp; Japanese.
PS
PS The present invention describes the high-concentration preparation of
CC soluble thrombomodulin. The present sequence represents a human soluble
CC thrombomodulin, which is given in the exemplification of the present
CC invention.
XX
XX Sequence 516 AA;
SQ
Query Match 100.0%; Score 2830; DB 7; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 78
QY 61 GGVRRRLWIGLQPLPGCGDPRKRLGFRQWVTGDNNTSYSRWARLDNGAPLCGLCV 120
Db 79 GGVRRRLWIGLQPLPGCGDPRKRLGFRQWVTGDNNTSYSRWARLDNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFHPCFATCRPLAVEPGAAAAVSIYGTPTFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFHPCFATCRPLAVEPGAAAAVSIYGTPTFA 198
QY 181 ARGADFOALFVGSSAAVAPLGLQIMCTAPPGVQGHWAREAPGAWDCSVENGCGEHCACNA 240
Db 199 ARGADFOALFVGSSAAVAPLGLQIMCTAPPGVQGHWAREAPGAWDCSVENGCGEHCACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQPGSYSCMCTGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQPGSYSCMCTGYRLAA 318
QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPFRANCEYQC 360
Db 319 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQACFADCDPNTQASCECPGYYILDGFI 420
Db 379 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQACFADCDPNTQASCECPGYYILDGFI 438
QY 421 CTDIDECENGFCGVCNHLPGTFCICGPDASALVRHIGTDCDQKVDGSGSGEPPPPS 480
Db 439 CTDIDECENGFCGVCNHLPGTFCICGPDASALVRHIGTDCDQKVDGSGSGEPPPPS 498
QY 481 FTGSGSTLTPPAVGLVHSG 498
Db 499 FTGSGSTLTPPAVGLVHSG 516
RESULT 9
AAR11534
ID AAR11534 standard; protein; 575 AA.
XX
XX AAR11534;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 17-JUN-1991 (first entry)

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XX Human thrombomodulin type II polypeptide.
DE
XX Thrombomodulin; chondroitin; protein C; thrombin; thrombolysis;
KW chondroitin sulphate; anticoagulant; myocardial infarction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Peptide /label= signal peptide
FT Peptide 19..365
FT Peptide /label= opt. N-terminal sequence
FT Peptide 366..480
FT Peptide /label= human thrombomodulin active fragment
FT Peptide 481..516
FT Peptide /label= opt. C-terminal sequence
PN W09104276-A.
XX
PD 04-APR-1991.
XX
PF 25-SEP-1989; 89JP-00246270.
XX
PR 25-SEP-1989; 89JP-00246270.
XX
PA (ASAH ) ASahi KASEI KOGYO KK.
XX
PI Yamamoto S, Gomi K, Ogawa K;
XX WPI; 1991-117478/16.
XX
DR New human thrombomodulin polypeptide contg. chondroitin - has
PT anticoagulant platelet agglutination and thrombolytic activity.
XX
PS Disclosure; Fig 1; 80pp; Japanese.
XX
CC This human thrombomodulin polypeptide comprises a 115 residue active
CC fragment with opt. flanking sequences (N-terminal= 347 amino acids; C-
CC terminal= 36 amino acids). Additionally it has an N-terminal signal
CC sequence and an attached sugar chain, contg. chondroitin or chondroitin
CC sulphate. It promotes the activation of protein C by thrombin and has
CC good anticoagulant, platelet aggregation inhibition and thrombolytic
CC activities. It can therefore be used for treating cardiovascular
CC diseases, eg arteriosclerosis or myocardial infarction. (Updated on 09-
CC JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 575 AA;
Query Match 100.0%; Score 2830; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.2e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 78
QY 61 GGVRRRLWIGLQPLPGCGDPRKRLGFRQWVTGDNNTSYSRWARLDNGAPLCGLCV 120
Db 79 GGVRRRLWIGLQPLPGCGDPRKRLGFRQWVTGDNNTSYSRWARLDNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFHPCFATCRPLAVEPGAAAAVSIYGTPTFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFHPCFATCRPLAVEPGAAAAVSIYGTPTFA 198
QY 181 ARGADFOALFVGSSAAVAPLGLQIMCTAPPGVQGHWAREAPGAWDCSVENGCGEHCACNA 240
Db 199 ARGADFOALFVGSSAAVAPLGLQIMCTAPPGVQGHWAREAPGAWDCSVENGCGEHCACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQPGSYSCMCTGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCHEFCVNPDPQPGSYSCMCTGYRLAA 318

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QY 301 DOHRCEDVDDCILEPSPQPCVNTQGGFECHYPNYDLVDGECVEPVDPCFRANCEYQC 360
 DB 319 DOHRCEDVDDCILEPSPQPCVNTQGGFECHYPNYDLVDGECVEPVDPCFRANCEYQC 378
 QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYIILDDGFI 420
 DB 379 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYIILDDGFI 438
 QY 421 CTIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDSKVDGSGSGGEPPEPS 480
 DB 439 CTIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDSKVDGSGSGGEPPEPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 DB 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 10
 AAR41806
 ID AAR41806 standard; peptide; 575 AA.
 XX AC AAR41806;
 XX 30-MAR-1994 (first entry)
 DT 30-MAR-1994 (first entry)
 DE Thrombomodulin.
 KW Transformation; fungus; blood coagulation; prevention; platelet;
 KW aggregation; thrombolytic activity; thrombolysis; human thrombomodulin;
 KW site-directed mutagenesis; promotion; protein C; activation; thrombin.
 OS Homo sapiens.
 XX XX JP05213998-A.
 XX 24-AUG-1993.
 XX 02-AUG-1991; 91JP-00282369.
 XX 03-AUG-1990; 90JP-00204978.
 PR 30-JUL-1991; 91JP-00189984.
 XX (ASAH) ASAH CHEM IND CO LTD.
 PA WPI; 1993-299652/38.
 DR Novel polypeptide obtd. by culturing transformed fungus - having blood
 PT coagulation preventing, platelet aggregation preventing and thrombolytic
 PT activities.
 XX Disclosure; Fig 55; 65pp; Japanese.
 XX Novel polypeptides, obtd. by culturing transformed fungus, have blood
 CC coagulation preventing, platelet aggregation preventing and thrombolytic
 CC activities. In an example, plasmid M3mpl9TMD3 (constructed from pSV2TMJ2
 CC (ATCC 67238) contg. a human thrombomodulin sequence) was subjected to
 CC site directed mutagenesis to prepare pSV2TMD7. Plasmid pSV2TMD7 was
 CC transfected to COS-1 cells. The activity of promoting protein C
 CC activation by thrombin of the peptide produced by the transformed COS-1
 CC cell was measured. The amt. of the peptide was determined
 XX Sequence 575 AA;
 SQ

Query Match 100.0%; Score 2830; DB 2; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.2e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSGQVEHDCFALYPGPATFLINASQICDGLRGHLMTVRRSSVAADVISLLNGD 60
 DB 19 APAEPQGGSGQVEHDCFALYPGPATFLINASQICDGLRGHLMTVRRSSVAADVISLLNGD 78
 QY 61 GGVGRRRLWIGLQLPPGCGDPKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGPLCV 120

DB 79 GGVGRRRLWIGLQLPPGCGDPKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGPLCV 138
 QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAAASVITVGTTPA 180
 DB 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAAASVITVGTTPA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 240
 DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 258
 QY 241 IPGAPROCPCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCETGYRLAA 300
 DB 259 IPGAPROCPCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCETGYRLAA 318
 QY 301 DOHRCEDVDDCILEPSPQPCVNTQGGFECHYPNYDLVDGECVEPVDPCFRANCEYQC 360
 DB 319 DOHRCEDVDDCILEPSPQPCVNTQGGFECHYPNYDLVDGECVEPVDPCFRANCEYQC 378
 QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYIILDDGFI 420
 DB 379 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECPGYIILDDGFI 438
 QY 421 CTIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDSKVDGSGSGGEPPEPS 480
 DB 439 CTIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDSKVDGSGSGGEPPEPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 DB 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 11
 AAR43031
 ID AAR43031 standard; protein; 575 AA.
 XX AC AAR43031;
 XX 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX Human thrombomodulin.
 DE Anticoagulant; platelet aggregation inhibitor; protein C; activation;
 KW thrombin; thrombomodulin; coagulation disorder; thrombosis;
 KW myocardial infarction; embolism; telangiectasis;
 KW arteriosclerosis obliterans; disseminated intravascular coagulation; DIC;
 KW angina pectoris; gestosis; transient ischaemic attack.
 XX Homo sapiens.
 OS W09322447-A1.
 PN 11-NOV-1993.
 PD 30-APR-1993; 93WO-JP000578.
 XX 01-MAY-1992; 92JP-00112903.
 PR (ASAH) ASAH KASEI KOGYO KK.
 XX Zushi M, Kondo S, Toma K;
 XX WPI; 1993-368806/46.
 DR Peptide with anticoagulant and platelet aggregation inhibitor activity -
 XX which promotes protein C activation by thrombin and is useful in treating
 PT coagulation disorders e.g. thrombosis.
 PT Disclosure; Fig 1; 84pp; Japanese.
 PS New peptides (see AAR50069) are inhibitors of the blood coagulation and
 CC platelet aggregation activities of thrombin and promote the protein-C

CC activation effect of thrombin. They can be produced efficiently in pure
 CC form by culture of appropriate transformants, and are useful in treatment
 CC of circulatory disorders such as myocardial infarction, thrombosis,
 CC embolism, telangiectasis, arteriosclerosis obliterans, disseminated
 CC intravascular coagulation, angina pectoris, gestosis and transient
 CC ischaemic attack. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 575 AA;

Query Match 100.0%; Score 2830; DB 2; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.2e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSVAADVLSLLNGD 78
 QY 61 GGVGRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWRLDLNGAPLCPLCV 120
 Db 79 GGVGRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWRLDLNGAPLCPLCV 138
 QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAVSITGTPFA 180
 Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAVSITGTPFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCCACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCCACNA 258
 QY 241 IPGAPRCOPAGALQADGRSCITASQSCNDLCEHFCVNPDPQSGYSYSCMCTGYRLAA 300
 Db 259 IPGAPRCOPAGALQADGRSCITASQSCNDLCEHFCVNPDPQSGYSYSCMCTGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVEPVDPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVEPVDPCFRANCEYQC 378
 QY 361 QPLNQTSLVCVAEGFAPIPHEPHRCMFCNQACADCDPNTQASCPREGYIILDDGFI 420
 Db 379 QPLNQTSLVCVAEGFAPIPHEPHRCMFCNQACADCDPNTQASCPREGYIILDDGFI 438
 QY 421 CTDIDECENGFCGVCNHLGTFECICGPPSALVRHGTCDGSKVDGSGSGGEPSPS 480
 Db 439 CTDIDECENGFCGVCNHLGTFECICGPPSALVRHGTCDGSKVDGSGSGGEPSPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 12
 AAEL17521
 ID AAEL17521 standard; protein; 575 AA.
 AC AAEL17521;
 XX
 XX
 XX
 XX
 XX 22-APR-2002 (first entry)
 XX Human full-length native thrombomodulin (TM).
 DE Human; thrombomodulin; TM analogue; protein C; thrombotic disease;
 XX antithrombotic therapy; thrombin-activatable fibrinolysis inhibitor;
 KW TAFI; myocardial infarction; disseminated intravascular coagulation; DIC;
 KW deep vein thrombosis; septic shock; pulmonary embolism; angina;
 KW acute respiratory distress syndrome; cancer; toxemia; septicemia;
 KW circulatory disorder; coronary embolism; pulmonary embolism;
 KW systemic coagulation disorder; immunosuppressive; cerebroprotective;
 KW pregnancy; anticoagulant; thrombolytic; venous occlusive condition;
 KW antibacterial; cardiant.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers

FT Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..575
 FT /note= "Human mature thrombomodulin"
 FT Domain 19..244
 FT /label= N-terminal_domain
 FT Domain 245..480
 FT /note= "6 EGF-like domains"
 FT Modified-site 481..515
 FT /note= "O-linked glycosylation site"
 FT Domain 516..539
 FT /label= Transmembrane_domain
 FT Domain 540..575
 FT /label= Cytoplasmic_domain
 PN WO200198352-A2.
 PD 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019590.
 XX 21-JUN-2000; 2000US-0213678P.
 PR 12-JUN-2001; 2001US-00880484.
 XX (SCHD) SCHERING AG.
 PA Light D, Morser MJ, Nagashima M;
 PI WPI; 2002-154622/20.
 DR N-PSDB; AAD28182.
 XX
 XX Thrombomodulin analog with greater ability to potentiate thrombin-mediated activation of protein C and lesser ability to potentiate thrombin-mediated activation of thrombin-activatable fibrinolysis inhibitor for treating thrombotic disease.
 PS Claim 1; Fig 4; 53pp; English.

The invention relates to the design, production and use of thrombomodulin (TM) analogues that have the ability to enhance the thrombin-mediated activation of protein C which have a significantly reduced ability to promote activation of thrombin-activatable fibrinolysis inhibitor (TAFI). TM analogue is useful for treating thrombotic disease in human, by administering it or a polynucleotide encoding it to the patient and expressing the analogue in vivo. Composition comprising TM analogue is useful for treating a thrombotic disease or condition in mammals. TM analogue is useful in antithrombotic therapy. TM analogue is also useful for treating diseases in which thrombus formation plays a significant etiological role including myocardial infarction, disseminated intravascular coagulation (DIC), deep vein thrombosis, septic shock, pulmonary embolism, acute respiratory distress syndrome, unstable angina and other arterial or venous occlusive conditions. TM analogue is also useful for treating various circulatory disorders including coronary or pulmonary embolism, stroke and systemic coagulation disorders including DIC which is often associated with septicemia, certain cancers and toxemia of pregnancy. The present sequence is human full-length native thrombomodulin

SQ Sequence 575 AA;

Query Match 100.0%; Score 2830; DB 5; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.2e-149;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSVAADVLSLLNGD 78
 QY 61 GGVGRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWRLDLNGAPLCPLCV 120
 Db 79 GGVGRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWRLDLNGAPLCPLCV 138
 QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAVSITGTPFA 180

Db 139 AVSAEATVPSEPIWEEQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSIITGTTPA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGCEHACNA 258
 QY 241 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVPNPDPQGSYSVCMCETGYRLAA 300
 Db 259 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVPNPDPQGSYSVCMCETGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQPCQVCNTQGGFCHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCQVCNTQGGFCHCYPNYDLVDGECVEPVPDPCFRANCEYQC 378
 QY 361 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYIILDDGFI 420
 Db 379 QPLNQTSLVLCVCAEGFAPIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYIILDDGFI 438
 QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDCKGVDGSDSGSGEPPEPS 480
 Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDCKGVDGSDSGSGEPPEPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 13

AAE23026
 ID AAE23026 standard; protein; 575 AA.

AC AAE23026;

XX 21-AUG-2002 (first entry)
 XX Human thrombomodulin protein.

XX Human; thrombomodulin; analogue; neurologic trauma; vulnery;
 KW spinal cord injury; neurological damage; therapy; tranquilliser;
 KW neuroprotective.

XX Homo sapiens.

Key Location/Qualifiers
 FT Domain 1..226
 FT Peptide 1..18
 FT Protein 19..575
 FT Domain 227..462
 FT Modified-site 463..497
 FT Domain 498..521
 FT Domain 522..557
 FT Domain 558..575
 FT Domain 576..590
 FT Domain 591..605
 FT Domain 606..620
 FT Domain 621..635
 FT Domain 636..650
 FT Domain 651..665
 FT Domain 666..680
 FT Domain 681..695
 FT Domain 696..710
 FT Domain 711..725
 FT Domain 726..740
 FT Domain 741..755
 FT Domain 756..770
 FT Domain 771..785
 FT Domain 786..800
 FT Domain 801..815
 FT Domain 816..830
 FT Domain 831..845
 FT Domain 846..860
 FT Domain 861..875
 FT Domain 876..890
 FT Domain 891..905
 FT Domain 906..920
 FT Domain 921..935
 FT Domain 936..950
 FT Domain 951..965
 FT Domain 966..980
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WO200217953-A2.

07-MAR-2002.

31-AUG-2001; 2001WO-US041930.

31-AUG-2000; 2000US-0229714P.

23-AUG-2001; 2001US-00938405.

(SCHD) SCHERING AG.

Festoff BW, Morser MJ;

XX

DR WPI; 2002-415551/44.
 DR N-PSDB; AAD36901.

XX Treating neurological damage resulting from spinal cord injury in humans
 by administering a soluble, recombinant thrombomodulin analog which is
 resistant to oxidation.

XX Claim 1; Fig 1; 31pp; English.

XX The invention relates to a method of using thrombomodulin analogues in
 the treatment of the neurologic trauma associated with spinal cord injury
 in mammals. The method involves administering an oxidation resistant
 soluble, recombinant thrombomodulin analogue, where the methionine at
 position 388 has been replaced with a leucine, and the analogue is
 numbered in accordance with native thrombomodulin. The method and
 thrombomodulin analogue are useful for treating neurological damage
 resulting from spinal cord injury in human. The present sequence is human
 thrombomodulin protein

XX Sequence 575 AA;

Query Match 100.0%; Score 2830; DB 5; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.2e-149;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVISLLNGD 60
 Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVISLLNGD 78
 QY 61 GVGRRRLWIGLQPLPGCGDPKRLGFLRGFWMTGDNNTSYRWARLDLNGAPLCGLCV 120
 Db 79 GVGRRRLWIGLQPL

KW antithrombotic therapy; thrombin-activatable fibrinolysis inhibitor;
 KW TAFI; myocardial infarction; disseminated intravascular coagulation; DIC;
 KW deep vein thrombosis; septic shock; pulmonary embolism; angina;
 KW acute respiratory distress syndrome; cancer; toxemia; septicemia;
 KW circulatory disorder; coronary embolism; pulmonary embolism; stroke;
 KW systemic coagulation disorder; immunosuppressive; cerebroprotective;
 KW pregnancy; anticoagulant; thrombolytic; venous occlusive condition;
 KW antibacterial; cardiant; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 474
 FT /note= "Wild-type Ser substituted with Ala; This location
 FT corresponds to position 492 of native thrombomodulin"
 XX
 XX WO200198352-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-US019590.
 XX
 XX 21-JUN-2000; 2000US-0213678P.
 XX 12-JUN-2001; 2001US-00880484.
 XX
 XX (SCHD) SCHERING AG.
 XX
 XX Light D, Morser MJ, Nagashima M;
 XX WPI; 2002-154622/20.
 XX
 XX Thrombomodulin analog with greater ability to potentiate thrombin-
 XX mediated activation of protein C and lesser ability to potentiate
 XX thrombin-mediated activation of thrombin-activatable fibrinolysis
 XX inhibitor for treating thrombotic disease.
 XX
 XX Claim 11; Page; 53pp; English.
 XX
 XX The invention relates to the design, production and use of thrombomodulin
 XX (TM) analogues that have the ability to enhance the thrombin-mediated
 XX activation of protein C which have a significantly reduced ability to
 XX promote activation of thrombin-activatable fibrinolysis inhibitor (TAFI).
 XX TM analogue is useful for treating thrombotic disease in human, by
 XX administering it or a polynucleotide encoding it to the patient and
 XX expressing the analogue in vivo. Composition comprising TM analogue is
 XX useful for treating a thrombotic disease or condition in mammals. TM
 XX analogue is useful in antithrombotic therapy. TM analogue is also useful
 XX for treating diseases in which thrombus formation plays a significant
 XX etiological role including myocardial infarction, disseminated
 XX intravascular coagulation (DIC), deep vein thrombosis, septic shock,
 XX pulmonary embolism, acute respiratory distress syndrome, unstable angina
 XX and other arterial or venous occlusive conditions. TM analogue is also
 XX useful for treating various circulatory disorders including coronary or
 XX pulmonary embolism, stroke and systemic coagulation disorders including
 XX DIC which is often associated with septicemia, certain cancers and
 XX toxemia of pregnancy. The present sequence is human thrombomodulin
 XX mutant. Note: This sequence is not shown in the specification, but it is
 XX constructed based on human native thrombomodulin sequence SEQ.ID.NO.2
 XX shown in fig 4 of the specification
 XX
 XX Sequence 557 AA;
 XX
 XX Query Match 99.9%; Score 2827; DB 5; Length 557;
 XX Best Local Similarity 99.8%; Pred. No. 1.7e-149;
 XX Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 XX 1 APAEPQGGSCQVEHDCALYPGPATFELNASQICDGLRGLMTVRSSVAADVILLNGD 60
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 XX 1 APAEPQGGSCQVEHDCALYPGPATFELNASQICDGLRGLMTVRSSVAADVILLNGD 60
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 XX 61 GGVGRRRLWIGLQLPFGGDPKRLGFRQVWTDGNNNTSYSRWRLDLNGAPLCGLCV 120
 XX
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Db 61 GGVGRRRLWIGLQLPFGGDPKRLGFRQVWTDGNNNTSYSRWRLDLNGAPLCGLCV 120
 QY 121 AVSAEAATVPSEPIWEEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAAASITTYGTPFA 180
 Db 121 AVSAEAATVPSEPIWEEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAAASITTYGTPFA 180
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCCHEACNA 240
 Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCCHEACNA 240
 QY 241 IFGAPRCQCPAGAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGVRLAA 300
 Db 241 IFGAPRCQCPAGAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGVRLAA 300
 QY 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCGCEVPEVDPFCFRANCEYQC 360
 Db 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCGCEVPEVDPFCFRANCEYQC 360
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 Db 361 QPLNQTSYLVCACGFAPIPIPHPHRCOMFCNCTACPADCDNTQASCCEPGYIILDDGFI 420
 QY 421 CTDIDECENGFCGSGVCHNLPTFECICGPPDSALVRHIGTDCDSKVDGSGSGSEPPPS 480
 Db 421 CTDIDECENGFCGSGVCHNLPTFECICGPPDSALVRHIGTDCDSKVDGSGSGSEPPPS 480
 QY 481 PTPGSTLTTPPAVLVHSG 498
 Db 481 PTPGSTLTTPPAVLVHSG 498

RESULT 15

AAE17525

ID AAE17525 standard; protein; 557 AA.

AC AAE17525;

XX

DT 22-APR-2002 (first entry)

XX Human thrombomodulin (TM) mutant, M388L.

XX Human; thrombomodulin; TM analogue; protein C; thrombotic disease;
 KW antithrombotic therapy; thrombin-activatable fibrinolysis inhibitor;
 KW TAFI; myocardial infarction; disseminated intravascular coagulation; DIC;
 KW deep vein thrombosis; septic shock; pulmonary embolism; angina;
 KW acute respiratory distress syndrome; cancer; toxemia; septicemia;
 KW circulatory disorder; coronary embolism; pulmonary embolism; stroke;
 KW systemic coagulation disorder; immunosuppressive; cerebroprotective;
 KW pregnancy; anticoagulant; thrombolytic; venous occlusive condition;
 KW antibacterial; cardiant; mutant; mutein.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 388

XX /note= "Wild-type Met substituted with Leu; This location
 XX corresponds to position 406 of native thrombomodulin"

XX WO200198352-A2.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019590.

XX 21-JUN-2000; 2000US-0213678P.

XX 12-JUN-2001; 2001US-00880484.

XX (SCHD) SCHERING AG.

XX Light D, Morser MJ, Nagashima M;
 XX WPI; 2002-154622/20.

Search completed: June 9, 2004, 08:47:57
Job time: 56.5 secs

XX	Thrombomodulin analog with greater ability to potentiate thrombin-mediated activation of protein C and lesser ability to potentiate thrombin-mediated activation of thrombin-activatable fibrinolysis inhibitor for treating thrombotic disease.	Claim 11; Page: 53pp; English.
XX	The invention relates to the design, production and use of thrombomodulin (TM) analogues that have the ability to enhance the thrombin-mediated activation of protein C which have a significantly reduced ability to promote activation of thrombin-activatable fibrinolysis inhibitor (TAFI).	
XX	TM analogue is useful for treating thrombotic disease in human, by administering it or a polynucleotide encoding it to the patient and expressing the analogue in vivo. Composition comprising TM analogue is useful for treating a thrombotic disease or condition in mammals. TM analogue is useful in antithrombotic therapy. TM analogue is also useful for treating diseases in which thrombus formation plays a significant etiological role including myocardial infarction, disseminated intravascular coagulation (DIC), deep vein thrombosis, septic shock, pulmonary embolism, acute respiratory distress syndrome, unstable angina and other arterial or venous occlusive conditions. TM analogue is also useful for treating various circulatory disorders including coronary or pulmonary embolism, stroke and systemic coagulation disorders including DIC which is often associated with septicemia, certain cancers and toxemia of pregnancy. The present sequence is human thrombomodulin mutant. Note: This sequence is not shown in the specification, but it is constructed based on human native thrombomodulin sequence SEQ.ID.NO.2 shown in fig 4 of the specification	
XX	Sequence 557 AA;	
XX	Query Match 99.9%; Score 2827; DB 5; Length 557; Best Local Similarity 99.8%; Pred. No. 1.7e-149; Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
QY	1 APAPFPQGGSCQVCHDFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60	
Db	1 APAPFPQGGSCQVCHDFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60	
QY	61 GVGRRRLWIGLOIPPGCGDDPKRLPLRGFWMTGDNNTTSYRWARLDLNGAPLCGLCV 120	
Db	61 GVGRRRLWIGLOIPPGCGDDPKRLPLRGFWMTGDNNTTSYRWARLDLNGAPLCGLCV 120	
QY	121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCEPLAVEPGAAAAAYSYITGTPFA 180	
Db	121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCEPLAVEPGAAAAAYSYITGTPFA 180	
QY	181 ARGADFOALPVGSSAAVAPLGLOLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 240	
Db	181 ARGADFOALPVGSSAAVAPLGLOLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 240	
QY	241 IPGAPRCQCAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSCHWCETGYRLAA 300	
Db	241 IPGAPRCQCAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSCHWCETGYRLAA 300	
QY	301 DQHRCEVDVDCILLEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPCFRANCEYQC 360	
Db	301 DQHRCEVDVDCILLEPSPQRCVNTQGGFECHCYENYDLVDGECVEPVDPCFRANCEYQC 360	
QY	361 QPLNQTSYLVCVAGGFAPIPEPHRCQFCNQTACPADCDPNTQASCCEPGYILDDGFI 420	
Db	361 QPLNQTSYLVCVAGGFAPIPEPHRCQFCNQTACPADCDPNTQASCCEPGYILDDGFI 420	
QY	421 CTDIDECENGCGFCSGVCHNLPGTFECLCGPDSALVRHIGTDCDSKVDGSGSGSEPPPS 480	
Db	421 CTDIDECENGCGFCSGVCHNLPGTFECLCGPDSALVRHIGTDCDSKVDGSGSGSEPPPS 480	
QY	481 PTPGSLTTPPAVGLVHSG 498	
Db	481 PTPGSLTTPPAVGLVHSG 498	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:46:09 ; Search time 16.5 Seconds
(without alignments)
1558.166 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516

Perfect score: 2830

Sequence: 1 APAEPQGGSCQVEHDCFAL.....PSPTGSLTPPAVLVHSG 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgm2_6/ptodata/2/iaa/5B_COMB.pgp:*
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4: /cgm2_6/ptodata/2/iaa/6B_COMB.pgp:*
5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pgp:*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2830	100.0	498	2	US-08-733-564-2
2	2830	100.0	575	1	US-08-261-206A-59
3	2830	100.0	575	4	US-09-880-484D-2
4	2826	99.9	575	1	US-08-312-870-1
5	2826	99.9	575	6	5466668-6
6	2824	99.8	497	4	US-09-331-793-4
7	2820	99.6	497	1	US-08-312-870-3
8	2818	99.6	575	1	US-08-170-290A-54
9	2756.5	97.4	572	6	5256770-7
10	2684	94.8	476	1	US-08-014-723-1
11	2684	94.8	476	1	US-08-110-011A-1
12	2684	94.8	494	1	US-08-014-723-14
13	2684	94.8	494	1	US-08-110-011A-14
14	2682	94.8	476	1	US-08-014-723-2
15	2682	94.8	476	1	US-08-014-723-18
16	2682	94.8	476	1	US-08-110-011A-2
17	2682	94.8	476	1	US-08-110-011A-18
18	2682	94.8	494	1	US-08-014-723-16
19	2682	94.8	494	1	US-08-110-011A-16
20	2604	92.0	475	1	US-08-307-444A-1
21	2604	92.0	475	1	US-08-587-389-1
22	2600	91.9	475	1	US-08-307-444A-2
23	2600	91.9	475	1	US-08-587-389-2
24	2596	91.7	456	1	US-08-307-444A-3
25	2596	91.7	456	1	US-08-587-389-3
26	2592	91.6	456	1	US-08-307-444A-4
27	2592	91.6	456	1	US-08-587-389-4

28	2543	89.9	446	1	US-08-307-444A-5	Sequence 5, Appli
29	2543	89.9	446	1	US-08-587-389-5	Sequence 5, Appli
30	1617	57.1	275	1	US-08-312-870-7	Sequence 7, Appli
31	1159	41.0	215	1	US-08-312-870-5	Sequence 5, Appli
32	685	24.2	114	2	US-08-733-564-1	Sequence 1, Appli
33	685	24.2	115	1	US-08-312-870-9	Sequence 9, Appli
34	575	20.3	652	2	US-08-751-305-2	Sequence 2, Appli
35	566.5	20.0	492	4	US-09-724-864-39	Sequence 39, Appli
36	358	12.7	638	2	US-08-897-443-1	Sequence 1, Appli
37	352	12.4	58	1	US-08-261-206A-3	Sequence 3, Appli
38	350.5	12.4	915	4	US-09-907-794A-34	Sequence 34, Appli
39	350.5	12.4	915	4	US-09-905-125A-34	Sequence 34, Appli
40	350.5	12.4	915	4	US-09-902-775A-34	Sequence 34, Appli
41	331.5	11.7	1964	4	US-09-467-997-1	Sequence 1, Appli
42	328.5	11.6	956	2	US-08-897-443-3	Sequence 3, Appli
43	323	11.4	1253	3	US-08-479-722B-4	Sequence 4, Appli
44	320.5	11.3	2321	4	US-09-230-652-2	Sequence 2, Appli
45	320	11.3	1394	6	5177197-30	Patent No. 5177197

ALIGNMENTS

RESULT 1

US-08-733-564-2
; Sequence 2, Application US/08733564
; Patent No. 5916874
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, Kenji
; APPLICANT: MOCHIDA, Satoshi
; TITLE OF INVENTION: METHOD FOR TREATING LIVER INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA: US/08/733,564
; FILING DATE: 18 OCTOBER 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 0216-0362P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-733-564-2

Query Match 100.0%; Score 2830; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1e-192;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRVSVAADVLSLLNGD 60
Db 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRVSVAADVLSLLNGD 60
Qy 61 GGVRRLRWLGLQLPPGCGDKRLGRLRGFWTGDNNNTSYSRWKLDLNGAPLCGLICV 120

Db 61 GGVRRRLMIGLQLPPGCGDKELGFLRGFWVTGDNNTSYSRWARLDLNGAPLCPVC 120
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPAGAAAAVSIYGTTPA 180
Db 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPAGAAAAVSIYGTTPA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSCMCETGYRLAA 300
Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSCMCETGYRLAA 300
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Db 301 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFCHCYNPYDLVDGECVEPVPDPCFRANCEYQC 360
QY 361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECPGYIIDDGFI 420
Db 361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECPGYIIDDGFI 420
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDVGKVDGSGSGEPPPS 480
Db 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDVGKVDGSGSGEPPPS 480
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 481 PTPGSTLTTPPAVGLVHSG 498

RESULT 2

US-08-261-206A-59
; Sequence 59, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..575
OTHER INFORMATION: /label= protein
OTHER INFORMATION: /note= "human thrombomodulin"
US-08-261-206A-59

Query Match 100.0%; Score 2830; DB 1: Length 575;
Best Local Similarity 100.0%; Pred. No. 1.2e-192;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQPGSQCEVHDCFPALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
Db 19 APAEPQPGSQCEVHDCFPALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 78
QY 61 GGVRRRLMIGLQLPPGCGDKELGFLRGFWVTGDNNTSYSRWARLDLNGAPLCPVC 120
Db 79 GGVRRRLMIGLQLPPGCGDKELGFLRGFWVTGDNNTSYSRWARLDLNGAPLCPVC 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPAGAAAAVSIYGTTPA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPAGAAAAVSIYGTTPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSCMCETGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSCMCETGYRLAA 318
QY 301 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFCHCYNPYDLVDGECVEPVPDPCFRANCEYQC 360
Db 319 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFCHCYNPYDLVDGECVEPVPDPCFRANCEYQC 378
QY 361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECPGYIIDDGFI 420
Db 379 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECPGYIIDDGFI 438
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDVGKVDGSGSGEPPPS 480
Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCDVGKVDGSGSGEPPPS 498
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 3

US-09-880-484D-2
; Sequence 2, Application US/09880484D
; Patent No. 6632791
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagashima, Mariko
; APPLICANT: Moiser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSM1
; CURRENT APPLICATION NUMBER: US/09/880,484D
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/213,678
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

LENGTH: 575

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-484D-2

Query Match 100.0%; Score 2830; DB 4; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.2e-192;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHMTVSSVAADVLSLLNGD 60
DB 19 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHMTVSSVAADVLSLLNGD 78
QY 61 GGVGRRRLWIGLQLPFGCGDPRKRLGFRQFVNTGDNNTSYSRWRLDNLGAPLCPLCV 120
DB 79 GGVGRRRLWIGLQLPFGCGDPRKRLGFRQFVNTGDNNTSYSRWRLDNLGAPLCPLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVITYGTTPA 180
DB 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVITYGTTPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAAREAPGAWDCSVENGCGCHACNA 240
DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAAREAPGAWDCSVENGCGCHACNA 258
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPNDPFGSYSCMCETGYRLAA 300
DB 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPNDPFGSYSCMCETGYRLAA 318
QY 301 DOHRCEDVDDCILLESPPORCVNTQSGHCYNVLDVDCVEVPCFRANCEYQC 360
DB 319 DOHRCEDVDDCILLESPPORCVNTQSGHCYNVLDVDCVEVPCFRANCEYQC 378
QY 361 QPLNQTSLVCVCAEGFAPIPHEPRCOMFCNOTACPADCDNTQASCECPGYYLLDDGFI 420
DB 379 QPLNQTSLVCVCAEGFAPIPHEPRCOMFCNOTACPADCDNTQASCECPGYYLLDDGFI 438
QY 421 CTDIDECNGGFCGVCNHLNPTFECICGPDALVRHIGTDCDCKVDDGSGSGEPSPS 480
DB 439 CTDIDECNGGFCGVCNHLNPTFECICGPDALVRHIGTDCDCKVDDGSGSGEPSPS 498
QY 481 PTPGSTLTTPPAVGLVHSG 498
DB 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 4

US-08-312-870-1

Sequence 1, Application US/08312870

Patent No. 5639625

GENERAL INFORMATION:

APPLICANT: Carlson, Craig W.

INVENTOR: Esmon, Charles T.

TITLE OF INVENTION: Method for detecting antibodies to

TITLE OF INVENTION: Thrombomodulin in Patient

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: Richards, Medlock & Andrews

STREET: 1201 Elm Street, Suite 450

CITY: Dallas

STATE: Texas

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/312.870

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 19..575
US-08-312-870-1

Query Match 99.9%; Score 2826; DB 1; Length 575;

Best Local Similarity 99.8%; Pred. No. 2.4e-192;

Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHMTVSSVAADVLSLLNGD 60

DB 19 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHMTVSSVAADVLSLLNGD 78

QY 61 GGVGRRRLWIGLQLPFGCGDPRKRLGFRQFVNTGDNNTSYSRWRLDNLGAPLCPLCV 120

DB 79 GGVGRRRLWIGLQLPFGCGDPRKRLGFRQFVNTGDNNTSYSRWRLDNLGAPLCPLCV 138

QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVITYGTTPA 180

DB 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVITYGTTPA 198

QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAAREAPGAWDCSVENGCGCHACNA 240

DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAAREAPGAWDCSVENGCGCHACNA 258

QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPNDPFGSYSCMCETGYRLAA 300

DB 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPNDPFGSYSCMCETGYRLAA 318

QY 301 DOHRCEDVDDCILLESPPORCVNTQSGHCYNVLDVDCVEVPCFRANCEYQC 360

DB 319 DOHRCEDVDDCILLESPPORCVNTQSGHCYNVLDVDCVEVPCFRANCEYQC 378

QY 361 QPLNQTSLVCVCAEGFAPIPHEPRCOMFCNOTACPADCDNTQASCECPGYYLLDDGFI 420

DB 379 QPLNQTSLVCVCAEGFAPIPHEPRCOMFCNOTACPADCDNTQASCECPGYYLLDDGFI 438

QY 421 CTDIDECNGGFCGVCNHLNPTFECICGPDALVRHIGTDCDCKVDDGSGSGEPSPS 480

DB 439 CTDIDECNGGFCGVCNHLNPTFECICGPDALVRHIGTDCDCKVDDGSGSGEPSPS 498

QY 481 PTPGSTLTTPPAVGLVHSG 498

DB 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 5

5466668-6

Patent No. 5466668

APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; FLIGHT,

DAVID R.

TITLE OF INVENTION: SUPERIOR THROMBOMODULIN ANALOGS FOR

PHARMACEUTICAL USE

NUMBER OF SEQUENCES: 57

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/155,346

FILING DATE: 22-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 568,456
FILING DATE: 15-AUG-1990
APPLICATION NUMBER: 506,325
FILING DATE: 09-APR-1990
APPLICATION NUMBER: 406,941
FILING DATE: 13-SEP-1989
APPLICATION NUMBER: 345,374
FILING DATE: 28-APR-1989
SEQ ID NO: 6;
LENGTH: 575
546668-6

Query Match
Best Local Similarity 99.9%; Score 2826; DB 6; Length 575;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
DB 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 78
QY 61 GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPCLCV 120
DB 79 GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPCLCV 138
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DB 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAAASITYGTTPFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCACNA 240
DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCACNA 258
QY 241 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 259 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
QY 301 DQHRCEVDVDDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVPEVDFPCFRANCEYQC 360
DB 319 DQHRCEVDVDDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVPEVDFPCFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQTACPADCDPNTQASCEPGEYIILDDGFI 420
DB 379 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQTACPADCDPNTQASCEPGEYIILDDGFI 438
QY 421 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDVGKVDGSGSGEPSPS 480
DB 439 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDVGKVDGSGSGEPSPS 498
QY 481 PTPGSTLTTPPAVGLVHS 498
DB 499 PTPGSTLTTPPAVGLVHS 516

RESULT 6
US-09-331-793-4
Sequence 4, Application US/09331793
Patent No. 6500646
GENERAL INFORMATION:
APPLICANT: KURIYAMA, Shinichi
APPLICANT: HASEGAWA, Takashi
TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
FILE REFERENCE: 1110-253P
CURRENT APPLICATION NUMBER: US/09/331,793
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patent in version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-331-793-4

Query Match
99.8%; Score 2824; DB 4; Length 497;

Best Local Similarity 100.0%; Pred. No. 2.8e-192;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
DB 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
QY 61 GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPCLCV 120
DB 61 GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPCLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAAASITYGTTPFA 180
DB 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAAASITYGTTPFA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCACNA 240
DB 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCACNA 240
QY 241 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 241 IFGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
QY 301 DQHRCEVDVDDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVPEVDFPCFRANCEYQC 360
DB 301 DQHRCEVDVDDCILEPSPQRCVNTQGGFECHCYNYDLVDGECVPEVDFPCFRANCEYQC 360
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQTACPADCDPNTQASCEPGEYIILDDGFI 420
DB 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCMFCNQTACPADCDPNTQASCEPGEYIILDDGFI 420
QY 421 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDVGKVDGSGSGEPSPS 480
DB 421 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDVGKVDGSGSGEPSPS 480
QY 481 PTPGSTLTTPPAVGLVHS 497
DB 481 PTPGSTLTTPPAVGLVHS 497

RESULT 7
US-08-312-870-3
Sequence 3, Application US/08312870
Patent No. 5639625
GENERAL INFORMATION:
APPLICANT: Carlson, Craig W.
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Method for Detecting Antibodies to
TITLE OF INVENTION: Thrombomodulin in Patients
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,870
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-870-3

Query Match
Best Local Similarity 99.6%; Score 2820; DB 1; Length 497;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCVCHDFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 60
Db 1 APAEPQGGSCVCHDFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 60
QY 61 GGVRRRLWIGLQPLPGCGDKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 61 GGVRRRLWIGLQPLPGCGDKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSTTYGTPFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSTTYGTPFA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAMDCSVENGCGCEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAMDCSVENGCGCEHACNA 240
QY 241 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
Db 241 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
QY 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECCHYCNYPNDLVGCEVPEVDPFCFRANCEYQC 360
Db 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECCHYCNYPNDLVGCEVPEVDPFCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQFNCOTACPADCDPNTQASCECEPEGYILLDDGFI 420
Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQFNCOTACPADCDPNTQASCECEPEGYILLDDGFI 420
QY 421 CTDIDECENGFCGVCVCHNLPTFECICGPDALVRHIGTDCDSKGVGDGSGSGEPPPS 480
Db 421 CTDIDECENGFCGVCVCHNLPTFECICGPDALVRHIGTDCDSKGVGDGSGSGEPPPS 480

QY 481 PTPGSTLTTPPAVGLVHS 497
Db 481 PTPGSTLTTPPAVGLVHS 497

RESULT 8
US-08-170-290A-54
Sequence 54, Application US/08170290A
Patent No. 5702931
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Morser, Michael J.
APPLICANT: Zielesner, Laura R.
TITLE OF INVENTION: No. 5702931el Mutagenesis Methods and
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/170,290A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05573
FILING DATE: 01-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/724,237
FILING DATE: 01-JUL-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 11972-58-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-170-290A-54

Query Match
Best Local Similarity 99.6%; Score 2818; DB 1; Length 575;
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APAEPQGGSCVCHDFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 60
Db 19 APAEPQGGSCVCHDFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 78
QY 61 GGVRRRLWIGLQPLPGCGDKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVRRRLWIGLQPLPGCGDKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSTTYGTPFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHPATCRPLAVEPGAAAAVSTTYGTPFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAMDCSVENGCGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAMDCSVENGCGCEHACNA 258
QY 241 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
Db 259 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 318
QY 301 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECCHYCNYPNDLVGCEVPEVDPFCFRANCEYQC 360
Db 319 DQHRCEVDVDCILEPSPQPCQRCVNTQGGFECCHYCNYPNDLVGCEVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQFNCOTACPADCDPNTQASCECEPEGYILLDDGFI 420
Db 379 QPLNQTSLVCVCAEGFAPIPHEPHRCQFNCOTACPADCDPNTQASCECEPEGYILLDDGFI 438
QY 421 CTDIDECENGFCGVCVCHNLPTFECICGPDALVRHIGTDCDSKGVGDGSGSGEPPPS 480
Db 439 CTDIDECENGFCGVCVCHNLPTFECICGPDALVRHIGTDCDSKGVGDGSGSGEPPPS 498
QY 481 PTPGSTLTTPPAVGLVHS 498
Db 499 PTPGSTLTTPPAVGLVHS 516

RESULT 9
5256770-7
Patent No. 5256770
APPLICANT: GLASER, CHARLES B.; MORSER, MICHAEL J.; LIGHT,
DAVID R.
TITLE OF INVENTION: OXIDATION RESISTANT THROMBOMODULIN ANALOGS

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;
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/506,325
; FILING DATE: 09-APR-1990
; SEQ ID NO: 7:
; LENGTH: 572
; 5256770-7

Query Match          97.4%; Score 2756.5; DB 6; Length 572;
Best Local Similarity 98.4%; Pred. No. 1.9e-187;
Matches 490; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
   |||||
Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 78
   |||||

QY 61 GGVGRRRLWIGLQPLPGCGDKPKLGRFQWVTGDNNTSYSRWARLDNGAPLCPLCV 120
   |||||
Db 79 GGVG-RLWIGLQPLPGCGDKPKLGRFQWVTGDNNTSYSRWARLDNGAPLCPLCV 137
   |||||

QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPEA 180
   |||||
Db 138 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPEA 197
   |||||

QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 240
   |||||
Db 198 ARGADFOALPVGSSAAVAPLGLQLMCTA--GNVQGHWAREAPGAWDCSVENGCGEHCACNA 255
   |||||

QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
   |||||
Db 256 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 315
   |||||

QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDCGCVPEVDPGCFRANCEYQC 360
   |||||
Db 316 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDCGCVPEVDPGCFRANCEYQC 375
   |||||

QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQNTACPADCDPNTQASCECEPEGYLLDDGFI 420
   |||||
Db 376 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQNTACPADCDPNTQASCECEPEGYLLDDGFI 435
   |||||

QY 421 CTTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDSKVGDSGSGEPPPS 480
   |||||
Db 436 CTTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDSKVGDSGSGEPPPS 495
   |||||

QY 481 PTFGSTLTTPPAVGLVHSG 498
   |||||
Db 496 PTFGSTLTTPPAVGLVHSG 513
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```

```
RESULT 10
US-08-014-723-1
; Sequence 1, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSER: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCES/DOCKET NUMBER: 80-071-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248955 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-014-723-1

Query Match          94.8%; Score 2684; DB 1; Length 476;
Best Local Similarity 99.4%; Pred. No. 2.1e-182;
Matches 473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
   |||||
Db 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
   |||||

QY 61 GGVGRRRLWIGLQPLPGCGDKPKLGRFQWVTGDNNTSYSRWARLDNGAPLCPLCV 120
   |||||
Db 61 GGVGRRRLWIGLQPLPGCGDKPKLGRFQWVTGDNNTSYSRWARLDNGAPLCPLCV 120
   |||||

QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPEA 180
   |||||
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPEA 180
   |||||

QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 240
   |||||
Db 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 240
   |||||

QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
   |||||
Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
   |||||

QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDCGCVPEVDPGCFRANCEYQC 360
   |||||
Db 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDCGCVPEVDPGCFRANCEYQC 360
   |||||

QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQNTACPADCDPNTQASCECEPEGYLLDDGFI 420
   |||||
Db 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQNTACPADCDPNTQASCECEPEGYLLDDGFI 420
   |||||

QY 421 CTTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDSKVGDSGSGE 476
   |||||
Db 421 CTTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDSKVGDSGSGE 476
   |||||
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```
RESULT 11
US-08-110-011A-1
; Sequence 1, Application US/08110011A
; Patent No. 5354664
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
```

ADDRESSEE: P.C.
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/110,011A
 FILING DATE: 23-AUG-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5354664man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 80-073-0 DIV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)413-3000
 TELEFAX: (703)413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-110-011A-1

Query Match 94.8%; Score 2684; DB 1; Length 476;
 Best Local Similarity 99.4%; Pred. No. 2.1e-182;
 Matches 473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	APAEPPQGGSCVCHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60
Db	1	APAEPPQGGSCVCHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60
QY	61	GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV	120
Db	61	GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV	120
QY	121	AVSAEATVPSEPIWEEOCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPA	180
Db	121	AVSAEATVPSEPIWEEOCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPA	180
QY	181	ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCCHEACNA	240
Db	181	ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCCHEACNA	240
QY	241	IPGAPRCOCAGALQADGRSCTASATQSCNDLCSEHFCVNPDPQPGSYSCMCTGYRLAA	300
Db	241	IPGAPRCOCAGALQADGRSCTASATQSCNDLCSEHFCVNPDPQPGSYSCMCTGYRLAA	300
QY	301	DOHRCEDVDDCILLESPPCPCQRCVNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC	360
Db	301	DOHRCEDVDDCILLESPPCPCQRCVNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC	360
QY	361	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQACDNTQASCECPGYYLDDGFI	420
Db	361	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQACDNTQASCECPGYYLDDGFI	420
QY	421	CTDIDCEGFCGSGVCHNLPGTFECICGPDSALVHIGTDCDSKVDGSGSGE	476
Db	421	CTDIDCEGFCGSGVCHNLPGTFECICGPDSALVHIGTDCDSKVDGSGSGE	476

RESULT 12

US-08-014-723-14
 ; Sequence 14, Application US/08014723
 ; Patent No. 5273962
 ; GENERAL INFORMATION:
 ; APPLICANT: Doi, Takeshi

APPLICANT: Iwasaki, Akio
 APPLICANT: Saino, Yushi
 APPLICANT: Kimura, Shigeru
 APPLICANT: Ohkuchi, Masao
 TITLE OF INVENTION: Thrombin-Binding Substance and Process
 TITLE OF INVENTION: For Preparing the Same
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/014,723
 FILING DATE: 19930208
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5273962man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 80-071-0 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)413-3000
 TELEFAX: (703)413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 494 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-014-723-14

Query Match 94.8%; Score 2684; DB 1; Length 494;
 Best Local Similarity 99.4%; Pred. No. 2.2e-182;
 Matches 473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	APAEPPQGGSCVCHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60
Db	19	APAEPPQGGSCVCHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	78
QY	61	GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV	120
Db	79	GGVRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV	138
QY	121	AVSAEATVPSEPIWEEOCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPA	180
Db	139	AVSAEATVPSEPIWEEOCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPA	198
QY	181	ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCCHEACNA	240
Db	199	ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCCHEACNA	258
QY	241	IPGAPRCOCAGALQADGRSCTASATQSCNDLCSEHFCVNPDPQPGSYSCMCTGYRLAA	300
Db	259	IPGAPRCOCAGALQADGRSCTASATQSCNDLCSEHFCVNPDPQPGSYSCMCTGYRLAA	318
QY	301	DOHRCEDVDDCILLESPPCPCQRCVNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC	360
Db	319	DOHRCEDVDDCILLESPPCPCQRCVNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC	378
QY	361	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQACDNTQASCECPGYYLDDGFI	420
Db	379	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQACDNTQASCECPGYYLDDGFI	438
QY	421	CTDIDCEGFCGSGVCHNLPGTFECICGPDSALVHIGTDCDSKVDGSGSGE	476

Db 439 CTDIDECENGFCVCHNLPGTFCICGPDALSALVRHIGTDCDSKVDYSGSSE 494

RESULT 13

US-08-110-011A-14
; Sequence 14, Application US/08110011A
; Patent No. 5354664
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,011A
; FILING DATE: 23-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5354664man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-073-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-011A-14

Query Match 94.8%; Score 2684; DB 1; Length 494;
Best Local Similarity 99.4%; Pred. No. 2.2e-182;
Matches 473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 APAEPQPGSGQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVVISLLNGD 60
Db 19 APAEPQPGSGQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVVISLLNGD 78
QY 61 GGVRRRLWIGLQLPFGCGDPRKLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVRRRLWIGLQLPFGCGDPRKLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAAAASITGTFFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAAAASITGTFFA 198
QY 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAMDCSVENGSCCHACNA 240
Db 199 ARGADFQALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAMDCSVENGSCCHACNA 258
QY 241 IFGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSYCMCETGYRLAA 300
Db 259 IFGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSYCMCETGYRLAA 318
QY 301 DQHRCEVDVDCILFSPQRCQVNTQGGFECFCYNYDLVDGECVEPVDPCFRANCEYQC 360

Db 319 DQHRCEVDVDCILFSPQRCQVNTQGGFECFCYNYDLVDGECVEPVDPCFRANCEYQC 378
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECPGYYLDDGFI 420
Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECPGYYLDDGFI 438
QY 421 CTDIDECENGFCVCHNLPGTFCICGPDALSALVRHIGTDCDSKVDYSGSSE 476
Db 439 CTDIDECENGFCVCHNLPGTFCICGPDALSALVRHIGTDCDSKVDYSGSSE 494

RESULT 14

US-08-014-723-2
; Sequence 2, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-014-723-2

Query Match 94.8%; Score 2682; DB 1; Length 476;
Best Local Similarity 99.2%; Pred. No. 3e-182;
Matches 472; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Db 1 APAEPQPGSGQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVVISLLNGD 60
QY 61 GGVRRRLWIGLQLPFGCGDPRKLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 61 GGVRRRLWIGLQLPFGCGDPRKLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAAAASITGTFFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEFFHFPATCRPLAVEPGAAAAAASITGTFFA 180

QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPVAVQGHWAREAPGAWDCSVENGCCCHACNA 240
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Db 421 CTDIDECENGFCGVCNHLPGTFECICGPDLSALVRHIGTDCDSKVDGSGSGS 476

RESULT 15

US-08-014-723-18
; Sequence 18, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Okuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 469
; OTHER INFORMATION: /note= "acidic amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 470
; OTHER INFORMATION: /note= "acidic amino acid"
US-08-014-723-18

Query Match 94.8%; Score 2682; DB 1; Length 476;
Best Local Similarity 99.4%; Pred. No. 3e-182;
Matches 472; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 APAEPQGGSCVCEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
Db 1 APAEPQGGSCVCEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
QY 61 GGVGRRRLWIGLQLPFGCGDPRKLGPLRGFQWVTGDNNTSYSRWARLDLNGAPLCPLCV 120
Db 61 GGVGRRRLWIGLQLPFGCGDPRKLGPLRGFQWVTGDNNTSYSRWARLDLNGAPLCPLCV 120
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Db 121 AVSAAEATVPSEPTWEEOQCEVKADGFLCEHFPATCEPLAVEPAAAAAASITTYTFFA 180
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Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
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Db 301 DQHRCEVDVDCILLEPSPQPCQRCVNTQGGFECCHYCNYPYDIADGCEVPEVDPDPCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQFCNQTACPADCDPNTQASCECEGYIILDDGFI 420
Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQFCNQTACPADCDPNTQASCECEGYIILDDGFI 420
QY 421 CTDIDECENGFCGVCNHLPGTFECICGPDLSALVRHIGTDCDSKVDGSGSGS 475
Db 421 CTDIDECENGFCGVCNHLPGTFECICGPDLSALVRHIGTDCDSKVDGSGSGS 475

Search completed: June 9, 2004, 08:51:29
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:50:04 ; Search time 42 Seconds
(without alignments)

3335.873 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516

Perfect score: 2830

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
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7: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	100.0	575	9	US-09-938-405-2
2	2830	100.0	575	10	US-09-880-464-2
3	2830	100.0	575	14	US-10-438-648-2
4	2830	100.0	575	15	US-10-410-195-2
5	2826	99.9	575	14	US-10-150-440-3
6	2826	99.9	575	15	US-10-373-801-29
7	2826	99.9	631	14	US-10-150-440-1
8	2824	99.8	497	15	US-10-298-736-4
9	2815	99.5	575	15	US-10-094-886-196
10	1036	36.6	239	15	US-10-104-047-2759
11	731	25.8	418	12	US-10-427-805-2
12	711	25.1	397	12	US-10-427-805-3
13	578	20.4	645	14	US-10-029-386-33151
14	578	20.4	652	16	US-10-408-765A-1422
15	576	20.4	652	9	US-09-789-919-96

16	575	20.3	652	12	US-10-211-462-131	Sequence 131, App
17	575	20.3	652	14	US-10-021-660-83	Sequence 83, Appl
18	574	20.3	467	12	US-10-210-172-176	Sequence 176, App
19	574	20.3	757	12	US-09-918-715-177	Sequence 177, App
20	574	20.3	757	12	US-09-918-715-196	Sequence 196, App
21	574	20.3	757	15	US-10-262-445-107	Sequence 107, App
22	566.5	20.0	765	12	US-09-918-715-190	Sequence 190, App
23	566.5	20.0	765	12	US-09-918-715-291	Sequence 291, App
24	538	19.0	644	9	US-09-789-919-62	Sequence 62, Appl
25	538	19.0	644	9	US-09-789-919-73	Sequence 73, Appl
26	414	14.6	1574	12	US-09-825-751A-77	Sequence 77, Appl
27	374	13.2	2906	15	US-10-015-115-60	Sequence 60, Appl
28	368	13.0	1231	12	US-10-363-616-482	Sequence 482, App
29	367.5	13.0	1051	16	US-10-309-290-10	Sequence 10, Appl
30	367.5	13.0	1131	16	US-10-309-290-8	Sequence 8, Appl
31	367.5	13.0	1145	16	US-10-309-290-12	Sequence 12, Appl
32	367.5	13.0	1184	16	US-10-309-290-6	Sequence 6, Appl
33	367	13.0	2871	15	US-10-015-115-59	Sequence 59, Appl
34	365	12.9	2911	12	US-09-825-751A-68	Sequence 68, Appl
35	365	12.9	2911	15	US-10-295-027-162	Sequence 162, App
36	365	12.9	2911	16	US-10-408-765A-421	Sequence 421, App
37	363.5	12.8	2695	15	US-10-015-115-14	Sequence 14, Appl
38	363	12.8	1393	12	US-10-312-352-21	Sequence 21, Appl
39	363	12.8	2871	15	US-10-015-115-57	Sequence 57, Appl
40	363	12.8	3002	15	US-10-015-115-56	Sequence 56, Appl
41	363	12.8	3002	16	US-10-408-765A-195	Sequence 195, App
42	359.5	12.7	1218	15	US-10-161-493-102	Sequence 102, App
43	359	12.7	741	16	US-10-408-765A-1187	Sequence 1187, App
44	359	12.7	782	12	US-10-428-275-176	Sequence 176, App
45	359	12.7	794	11	US-09-833-245-1292	Sequence 1292, Ap

ALIGNMENTS

RESULT 1

US-09-938-405-2
; Sequence 2, Application US/09938405
; Patent No. US20020111296A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/09/938,405
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-405-2

Query Match	100.0%;	Score	2830;	DB	9;	Length	575;
Best Local Similarity	100.0%;	Pred. No.	5.7e-194;				
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Gaps	0;						
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QY	181	ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCCHEACNA	240				

Db 199 ARGADFOALPVGSSAAVPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGSCHEACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFVCPNPDPQPSYSCMCTGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFVCPNPDPQPSYSCMCTGYRLAA 318
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Db 319 DQHRCEVDVDDCILEPSPCPORCVNTQGGFECHCYPNYDLVDGECVBPVDPCCFRANCEYOC 378
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCNTACPADCDPNTQASCECEGYILDDGFI 420
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Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDPSALVRHIGTDCDSKVDGSGSGGEPFPS 498
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 499 PTPGSTLTTPPAVGLVHSG 516
RESULT 2
US-09-880-464-2
; Sequence 2, Application US/09880464
; Publication No. US20030011623A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: Improved Thrombomodulin Analogs
; CURRENT APPLICATION NUMBER: US/09/880,464
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/213,678
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-464-2

Query Match 100.0%; Score 2830; DB 10; Length 575;
Best Local Similarity 100.0%; Pred. No. 5.7e-194;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQPGSGQCVHEHDFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVVISLLNGD 60
Db 19 APAEPQPGSGQCVHEHDFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVVISLLNGD 78
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGFLRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 120
Db 79 GGVGRRRLWIGLQLPFGCGDPKRLGFLRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
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QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDPSALVRHIGTDCDSKVDGSGSGGEPFPS 480
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QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 499 PTPGSTLTTPPAVGLVHSG 516
RESULT 3
US-10-438-648-2
; Sequence 2, Application US/10438648
; Publication No. US20030186883A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagashima, Mariko
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSD1
; CURRENT APPLICATION NUMBER: US/10/438,648
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 60/213,678
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/880,484
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-438-648-2

Query Match 100.0%; Score 2830; DB 14; Length 575;
Best Local Similarity 100.0%; Pred. No. 5.7e-194;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQPGSGQCVHEHDFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVVISLLNGD 60
Db 19 APAEPQPGSGQCVHEHDFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVVISLLNGD 78
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGFLRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 120
Db 79 GGVGRRRLWIGLQLPFGCGDPKRLGFLRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
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Db 319 DQHRCEVDVDDCILEPSPCPORCVNTQGGFECHCYPNYDLVDGECVBPVDPCCFRANCEYOC 378
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCNTACPADCDPNTQASCECEGYILDDGFI 420
Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCNTACPADCDPNTQASCECEGYILDDGFI 438
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDPSALVRHIGTDCDSKVDGSGSGGEPFPS 480
Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDPSALVRHIGTDCDSKVDGSGSGGEPFPS 498

```
Qy 481 PTPGSLTPPAVLVHSG 498
Db 499 PTPGSLTPPAVLVHSG 516

RESULT 4
US-10-410-195-2
; Sequence 2, Application US/10410195
; Publication No. US20040002446A1
; GENERAL INFORMATION:
; APPLICANT: Pestoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/10/410,195
; CURRENT FILING DATE: 2003-08-10
; PRIOR APPLICATION NUMBER: US/09/938,405
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-195-2

Query Match 100.0%; Score 2830; DB 15; Length 575;
Best Local Similarity 100.0%; Pred. No. 5,7e-194;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APAEPQGGSCVCHDCFCALYPGPATFLNASQICDGLRGHLMTVRSVAADVISILLNGD 60
Db 19 APAEPQGGSCVCHDCFCALYPGPATFLNASQICDGLRGHLMTVRSVAADVISILLNGD 78
Qy 61 GVGRRRLWIGLQPLPGCGDPKRLGRLGFGQVMTGDNNTSYRWARLDLNGAPLCGLCV 120
Db 79 GVGRRRLWIGLQPLPGCGDPKRLGRLGFGQVMTGDNNTSYRWARLDLNGAPLCGLCV 138
Qy 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTFFA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTFFA 198
Qy 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGECHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGECHACNA 258
Qy 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
Qy 301 DOHRCEDVDDCILPEPSPQRCVNTQGGFECHYCNPDNTQASCECEGYILLDDGFI 420
Db 319 DOHRCEDVDDCILPEPSPQRCVNTQGGFECHYCNPDNTQASCECEGYILLDDGFI 438
Qy 421 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSGSGSEPPPS 480
Db 439 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSGSGSEPPPS 498
Qy 481 PTPGSLTPPAVLVHSG 498
Db 499 PTPGSLTPPAVLVHSG 516

RESULT 5
US-10-150-440-3
; Sequence 3, Application US/10150440
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; Publication No. US20030022249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Juergen
; APPLICANT: Dzionek, Andrzej
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; TITLE OF INVENTION: A SUBSET OF DENDRITIC CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 212302001200
; CURRENT APPLICATION NUMBER: US/10/150,440
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-3

Query Match 99.9%; Score 2826; DB 14; Length 575;
Best Local Similarity 99.8%; Pred. No. 1.1e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APAEPQGGSCVCHDCFCALYPGPATFLNASQICDGLRGHLMTVRSVAADVISILLNGD 60
Db 19 APAEPQGGSCVCHDCFCALYPGPATFLNASQICDGLRGHLMTVRSVAADVISILLNGD 78
Qy 61 GVGRRRLWIGLQPLPGCGDPKRLGRLGFGQVMTGDNNTSYRWARLDLNGAPLCGLCV 120
Db 79 GVGRRRLWIGLQPLPGCGDPKRLGRLGFGQVMTGDNNTSYRWARLDLNGAPLCGLCV 138
Qy 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTFFA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTFFA 198
Qy 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGECHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGECHACNA 258
Qy 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
Qy 301 DOHRCEDVDDCILPEPSPQRCVNTQGGFECHYCNPDNTQASCECEGYILLDDGFI 420
Db 319 DOHRCEDVDDCILPEPSPQRCVNTQGGFECHYCNPDNTQASCECEGYILLDDGFI 438
Qy 361 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPDNDNTQASCECEGYILLDDGFI 420
Db 379 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPDNDNTQASCECEGYILLDDGFI 438
Qy 421 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSGSGSEPPPS 480
Db 439 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSGSGSEPPPS 498
Qy 481 PTPGSLTPPAVLVHSG 498
Db 499 PTPGSLTPPAVLVHSG 516
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RESULT 6
US-10-373-801-29
; Sequence 29, Application US/10373801
; Publication No. US20040005644A1
; GENERAL INFORMATION:
; APPLICANT: Yibai Pharmaceutical (USA)
; TITLE OF INVENTION: Method and composition for detection and treatment of breast cancer
; FILE REFERENCE: 12399-00
; CURRENT APPLICATION NUMBER: US/10/373,801
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-801-29

Query Match          99.9%; Score 2826; DB 15; Length 575;
Best Local Similarity 99.8%; Pred. No. 1.1e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 60
Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 78
QY 61 GGVRRRLWIGLQIPGCGDKPKLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVRRRLWIGLQIPGCGDKPKLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAVSITYGTTPA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAVSITYGTTPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 258
QY 241 IPGAPRCQCPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQPGSYSCMCEYGLAA 300
Db 259 IPGAPRCQCPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQPGSYSCMCEYGLAA 318
QY 301 DQHRCEVDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCVPEVDPFCFRANCEYQC 360
Db 319 DQHRCEVDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECEGYLLDDGFI 420
Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECEGYLLDDGFI 438
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDSKGVGDSGSGSEPPPS 480
Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDSKGVGDSGSGSEPPPS 498
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 7
US-10-150-440-1
; Sequence 1, Application US/10150440
; Publication No. US20030022249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Juergen
; APPLICANT: Dzionek, Andrzej
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; TITLE OF INVENTION: A SUBSET OF DENDRITIC CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 212302001200
; CURRENT APPLICATION NUMBER: US/10/150,440

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; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-1

Query Match          99.9%; Score 2826; DB 14; Length 631;
Best Local Similarity 99.8%; Pred. No. 1.2e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 60
Db 75 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 134
QY 61 GGVRRRLWIGLQIPGCGDKPKLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 135 GGVRRRLWIGLQIPGCGDKPKLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV 194
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAVSITYGTTPA 180
Db 195 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAVSITYGTTPA 254
QY 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 240
Db 255 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 314
QY 241 IPGAPRCQCPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQPGSYSCMCEYGLAA 300
Db 315 IPGAPRCQCPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQPGSYSCMCEYGLAA 374
QY 301 DQHRCEVDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCVPEVDPFCFRANCEYQC 360
Db 375 DQHRCEVDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDCVPEVDPFCFRANCEYQC 434
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECEGYLLDDGFI 420
Db 435 QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECEGYLLDDGFI 494
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDSKGVGDSGSGSEPPPS 480
Db 495 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALVRHIGTDCDSKGVGDSGSGSEPPPS 554
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 555 PTPGSTLTTPPAVGLVHSG 572

RESULT 8
US-10-298-796-4
; Sequence 4, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi

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;/ TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
;/ FILE REFERENCE: 1110-253P
;/ CURRENT APPLICATION NUMBER: US/10/298,796
;/ CURRENT FILING DATE: 2002-11-19
;/ PRIOR APPLICATION NUMBER: US/09/331,793
;/ PRIOR FILING DATE: 1999-06-25
;/ NUMBER OF SEQ ID NOS: 67
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 4
;/ LENGTH: 497
;/ TYPE: PRT
;/ ORGANISM: Homo Sapiens
;/ US-10-298-796-4

Query Match 99.8%; Score 2824; DB 15; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-193; Indels 0; Gaps 0;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APAEPQGGSCQVHEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
Db 1 APAEPQGGSCQVHEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
QY 61 GGVRRLWIGLQPPGCGDPKRLGPRGFWVTGDNNTSYSRWRLDNGAPLPGPLCV 120
Db 61 GGVRRLWIGLQPPGCGDPKRLGPRGFWVTGDNNTSYSRWRLDNGAPLPGPLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
QY 181 ARGADPQALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 181 ARGADPQALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPNDQPGSYSCMCTGYRLAA 300
Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPNDQPGSYSCMCTGYRLAA 300
QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDGECVPEVPDPCFRANCEYOC 360
Db 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYPNYDLVDGECVPEVPDPCFRANCEYOC 360
QY 361 QPLNQTSLYLCVCAEGFAPLPHBPHRCQMFNQTACDNPNTQASCEPEGYLLDDGFI 420
Db 361 QPLNQTSLYLCVCAEGFAPLPHBPHRCQMFNQTACDNPNTQASCEPEGYLLDDGFI 420
QY 421 CTDIDECENGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDSKGVGDGSGSGEPFPPS 480
Db 421 CTDIDECENGFCGVCNHLPGTFECICGPDSSALVRHIGTDCDSKGVGDGSGSGEPFPPS 480
QY 481 PTPGSTLTTPPVGVLVHS 497
Db 481 PTPGSTLTTPPVGVLVHS 497

RESULT 9
US-10-094-886-196
; Publication 196, Application US/10094886
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh

;/ APPLICANT: Padigar, Muralidhara
;/ APPLICANT: Taupier, Raymond J., Jr.
;/ APPLICANT: Miller, Charles
;/ APPLICANT: Casman, Stacie
;/ APPLICANT: Pena, Carol
;/ APPLICANT: Gangolli, Bsha
;/ APPLICANT: Gusev, Vladimir
;/ APPLICANT: Smithson, Glennda
;/ APPLICANT: Zernhusen, Bryan
;/ APPLICANT: Gerlach, Valerie
;/ APPLICANT: Pochart, Pascal
;/ APPLICANT: Fernandes, Elma
;/ APPLICANT: Shinkets, Richard
;/ APPLICANT: Rastelli, Luca
;/ APPLICANT: Spaderna, Steven
;/ APPLICANT: Larochele, William
;/ APPLICANT: Zhong, Mei
;/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;/ FILE REFERENCE: 21402-290 B
;/ CURRENT APPLICATION NUMBER: US/10/094,886
;/ CURRENT FILING DATE: 2002-03-07
;/ PRIOR APPLICATION NUMBER: 60/274,322
;/ PRIOR FILING DATE: 2001-03-08
;/ PRIOR APPLICATION NUMBER: 60/313,182
;/ PRIOR FILING DATE: 2001-08-17
;/ PRIOR APPLICATION NUMBER: 60/288,052
;/ PRIOR FILING DATE: 2001-05-02
;/ PRIOR APPLICATION NUMBER: 60/318,510
;/ PRIOR FILING DATE: 2001-09-10
;/ PRIOR APPLICATION NUMBER: 60/274,281
;/ PRIOR FILING DATE: 2001-03-08
;/ PRIOR APPLICATION NUMBER: 60/314,018
;/ PRIOR FILING DATE: 2001-08-21
;/ PRIOR APPLICATION NUMBER: 60/274,194
;/ PRIOR FILING DATE: 2001-03-08
;/ PRIOR APPLICATION NUMBER: 60/274,849
;/ PRIOR FILING DATE: 2001-03-09
;/ PRIOR APPLICATION NUMBER: 60/296,693
;/ PRIOR FILING DATE: 2001-06-07
;/ PRIOR APPLICATION NUMBER: 60/313,626
;/ PRIOR FILING DATE: 2001-08-21
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 298
;/ SOFTWARE: PatentIn 2.1
;/ SEQ ID NO 196
;/ LENGTH: 575
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ US-10-094-886-196

Query Match 99.5%; Score 2815; DB 15; Length 575;
Best Local Similarity 99.4%; Pred. No. 6.7e-193;
Matches 495; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVHEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
Db 19 APAEPQGGSCQVHEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 78
QY 61 GGVRRLWIGLQPPGCGDPKRLGPRGFWVTGDNNTSYSRWRLDNGAPLPGPLCV 120
Db 79 GGVRRLWIGLQPPGCGDPKRLGPRGFWVTGDNNTSYSRWRLDNGAPLPGPLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPFA 198
QY 181 ARGADPQALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 199 ARGADPQALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPNDQPGSYSCMCTGYRLAA 300
Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPNDQPGSYSCMCTGYRLAA 318

QY 301 DOHRCEVDVDDCILEPSPQRCVNTQGGFECHCYPNYDLVDGCEVPVDPFCFRANCEYOC 360
 Db 319 DQHRCEVDVDDCILEPSPQRCVNTQGGFECHCYPNYDLVDGCEVPVDPFCFRANCEYOC 378
 QY 361 QPLNQTSYLVCVCAEGFAPIPHEPFRQMFNQTACPADCDPNTQASCECEGYYLDDGFI 420
 Db 379 QPLNQTSYLVCVCAEGFAPIPHEPFRQMFNQTACPADCDPNTQASCECEGYYLDDGFI 438
 QY 421 CTDIDCEGNGFCGSGVCHNLPGTFECICGPDSDALVRHIGTDCDVGKVDGSGSGEPPPS 480
 Db 439 CTDIDCEGNGFCGSGVCHNLPGTFECICGPDSDALVRHIGTDCDVGKVDGSGSGEPPPS 498
 QY 481 PTPGSTLTTPPAVLVHSG 498
 Db 499 PTPGSTLTTPPAVLVHSG 516

RESULT 10

US-10-104-047-2759
 ; Sequence 2759, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2759
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-2759

Query Match 36.6%; Score 1036; DB 15; Length 239;
 Best Local Similarity 86.5%; Pred. No. 3.1e-66;
 Matches 180; Conservative 0; Mismatches 0; Indels 28; Gaps 1;
 QY 291 MCETGYRLAADOHRCEVDVDDCILEPSPQRCVNTQGGFECHCYPNYDLVDGCEVPVDP 350
 Db 1 MCETGYRLAADOHRCEVDVDDCILEPSPQRCVNTQGGFECHCYPNYDLVDGCEVPVDP 60
 QY 351 CFRANCEYOCQPLNQTSYLVCVCAEGFAPIPHEPFRQMFNQTACPADCDPNTQASCECP 410
 Db 61 CFRANCEYOCQPLNQTSYLVCVCAEGFAPIPHEPFRQMFNQTACPADCDPNTQASCE-- 118
 QY 411 EGYLDDGFICTDIDCEGNGFCGSGVCHNLPGTFECICGPDSDALVRHIGTDCDVGKVDG 470
 Db 119 -----CHNLPGTFECICGPDSDALVRHIGTDCDVGKVDG 152
 QY 471 DSGSGEPPSPTPGSTLTTPPAVLVHSG 498
 Db 153 DSGSGEPPSPTPGSTLTTPPAVLVHSG 180

RESULT 11

US-10-427-805-2
 ; Sequence 2, Application US/10427805
 ; Publication No. US20040063632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McLean, Kirk
 ; TITLE OF INVENTION: No. US20040063632A1 Tissue Factor Targeted Thrombomodulin Fusio
 ; FILE REFERENCE: 52295AUSM1
 ; CURRENT APPLICATION NUMBER: US/10/427,805
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/376,566
 ; PRIOR FILING DATE: 2002-05-01

; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456 fusion protein
 US-10-427-805-2

Query Match 25.1%; Score 711; DB 12; Length 418;
 Best Local Similarity 50.2%; Pred. No. 3.6e-44;
 Matches 148; Conservative 18; Mismatches 56; Indels 73; Gaps 8;
 QY 243 GAPRCQCPAGALOAD-GRSCTASATQSCNDLCEHFVCPNPDPQGSYSYCMCETGYRLAAD 301
 Db 150 GAPNFMLTQPHSVASPGKTVITISCTRSSGVSASYVOWYQORPGSSPTTV-----IYED 204
 QY 302 QHRCEVDVDDCILEPSPQRCVNT-----CVNT-----OGFECCHCYPNYDLV-- 340
 Db 205 NHR-----PSGVDPDRFGSITDTSNSASLTISGLKTEDEADYYCQSDSNLVVF 254
 QY 341 -----DGEVPEVDPFCFRANCEYOCQPLNQTSYLVCVCAEGF 376
 Db 255 GGGTCKLTVLGAAAGGGGGGGGGGSGVPEVDPFCFRANCEYOCQPLNQTSYLVCVCAEGF 314
 QY 377 APIPEPFRQMFNQTACPADCDPNTQASCECEGYYLDDGFICTDIDCEGNGFCGSGV 436
 Db 315 APIPEPFRQMFNQTACPADCDPNTQASCECEGYYLDDGFICTDIDCEGNGFCGSGV 374
 QY 437 CHNLPGTFECICGPDSDALVRHIGTDCDVGKVDGSGSGEPPSPTPGSTLTTPPA 491
 Db 375 CHNLPGTFECICGPDSDALVAGIQTDC-----AAAGAPVYPDP---LEPRA 417

RESULT 12

US-10-427-805-3
 ; Sequence 3, Application US/10427805
 ; Publication No. US20040063632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Light, David
 ; APPLICANT: McLean, Kirk
 ; TITLE OF INVENTION: No. US20040063632A1 Tissue Factor Targeted Thrombomodulin Fusio
 ; FILE REFERENCE: 52295AUSM1
 ; CURRENT APPLICATION NUMBER: US/10/427,805
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/376,566
 ; PRIOR FILING DATE: 2002-05-01
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 397
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456delta fusio
 US-10-427-805-3

Query Match 25.1%; Score 711; DB 12; Length 397;
 Best Local Similarity 54.6%; Pred. No. 9.1e-43;
 Matches 136; Conservative 14; Mismatches 39; Indels 60; Gaps 5;
 QY 259 GRSCTASATQSCNDLCEHFVCPNPDPQGSYSYCMCETGYRLAADQHRCEVDVDDCILEPSPC 318
 Db 164 GKTVTISCTRSSGVSASYVOWYQORPGSSPTTV-----IYEDNHR-----PSGV 208
 QY 319 POR---CVNT-----OGFECCHCYPNYDLV----- 340
 Db 209 PDRFGSITDTSNSASLTISGLKTEDEADYYCQSDSNLVVFGGTTKLTVLGAAGGG 268
 QY 341 -----DGEVPEVDPFCFRANCEYOCQPLNQTSYLVCVCAEGFAPIPHEPFRQMFNQT 393

Db 269 SGGGGGGGSGVDFVDFPCFRANCEYQCOPLNQTSYLVCVCAEGFAP1PHEPHRCQMFNCQT 328
QY 394 ACADCDPNTQASCECEGYLLDDGFTCTDIDCECGGCGSGVCHNLPGTFECICGPDSA 453
Db 329 ACADCDPNTQASCECEGYLLDDGFTCTDIDCECGGCGSGVCHNLPGTFECICGPDSA 388
QY 454 LVRHIGTDC 462
Db 389 LAGQIGTDC 397

RESULT 13

US-10-029-386-33151
; Sequence 33151, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33151
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL18508.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUOE 7.00e-44
US-10-029-386-33151

Query Match 20.4%; Score 578; DB 14; Length 645;
Best Local Similarity 31.6%; Pred. No. 4.9e-33;
Matches 175; Conservative 52; Mismatches 201; Indels 126; Gaps 31;

QY 6 QPGGSG-----CUEHDCFALYPGATFLNASQICDGLRHLMTVRSSVAAD-----VI 53
Db 17 QPGAGTGADTEAVVCGTACTYTAHSGKLSAAEAQNHCNQGNGNLATVKSKEEAQHVRVL 76
QY 54 SILLNGDGGVGR--RLWIGLQLPFG--CGDPKRLGRLGFOWVTGNNVTSYSRWALDLN 110
Db 77 AQLRREALTARMSKFWIGLQREKGLDPSL--PLKGF5WVGGEPTPYSNWHKELRN 134
QY 111 GAPLCGPLCVA--VSAAEATVPSE--PIWEEQOC-----EVKADGFLCFEHPATCRPLA 161
Db 135 SC--ISKRCVSLLLDLSQPLLPRLPKWSEGPCGSPGSGNIEGVFKFSFGKMCRLPLA 192
QY 162 V-EPGAAAASVITYGTPFAARGADFOALPVGSSAAVAPLGLQLMC--TAPPGAUVQGHW-- 217
Db 193 LGPG-----QVYTTPTPQTSSSLEAVPFAAANVA-----CGEGDKDETQSHYFL 239
QY 218 -AREAPGAWD-----CSVENGGCEHAC--NAIPGAPRCQCPAGALQADGRS 261
Db 240 CKEAPADVFWGSSGPLCVSPKYGNFNNGGCHQDCFEFGDGSFLCGCRPFGLLDLVT 299
QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSKCMETGYRLAADQHRCEVDVDDCILEPSPCP 319
Db 300 C-ASRNPSSSPCRGGATCVLGP-HGKNYTCRPGYQLDSSQLDCVDVDEC--QDSPCA 355
QY 320 QRCVNTQGGFECHCYNDYLDVGECEVPEVDFPCFRANCEYQCOPLNQTSYLVCVCAEGFAP1 379
Db 356 QECVNTPGGFRCECWGY-----EPGPP-----GEGACQDVDE-----CALGRSP- 395
QY 380 PHEPHRCQMFNCQACPADCDPNTQAS--CECEGYIL--DDGFICTDIDEC--ENGGEFC 433
Db 396 -----CAQGC--TNTDGSFHCSCGEGYVLAGEDGTQCQDVDCVGGGGLC 439

QY 434 SGVCHNLPGTFECICGPDGALVRHIGTDCDSGKV-----DGGDSGSGE-----P 477
Db 440 DSLCFNTQGSFHCGLPFGWVLAPE--GVSCCTMGFVSLGPPSGPPDEEDKGEKSGSTVPRAA 498
QY 478 PPSPTPGSTLTTPA 491
Db 499 TASPTRGPEGTAKA 512

RESULT 14

US-10-408-765A-1422
; Sequence 1422, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1422
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1422

Query Match 20.4%; Score 578; DB 16; Length 652;
Best Local Similarity 31.6%; Pred. No. 5e-33;
Matches 175; Conservative 52; Mismatches 201; Indels 126; Gaps 31;

QY 6 QPGGSG-----CUEHDCFALYPGATFLNASQICDGLRHLMTVRSSVAAD-----VI 53
Db 17 QPGAGTGADTEAVVCGTACTYTAHSGKLSAAEAQNHCNQGNGNLATVKSKEEAQHVRVL 76
QY 54 SILLNGDGGVGR--RLWIGLQLPFG--CGDPKRLGRLGFOWVTGNNVTSYSRWALDLN 110
Db 77 AQLRREALTARMSKFWIGLQREKGLDPSL--PLKGF5WVGGEPTPYSNWHKELRN 134
QY 111 GAPLCGPLCVA--VSAAEATVPSE--PIWEEQOC-----EVKADGFLCFEHPATCRPLA 161
Db 135 SC--ISKRCVSLLLDLSQPLLPRLPKWSEGPCGSPGSGNIEGVFKFSFGKMCRLPLA 192
QY 162 V-EPGAAAASVITYGTPFAARGADFOALPVGSSAAVAPLGLQLMC--TAPPGAUVQGHW-- 217
Db 193 LGPG-----QVYTTPTPQTSSSLEAVPFAAANVA-----CGEGDKDETQSHYFL 239
QY 218 -AREAPGAWD-----CSVENGGCEHAC--NAIPGAPRCQCPAGALQADGRS 261
Db 240 CKEAPADVFWGSSGPLCVSPKYGNFNNGGCHQDCFEFGDGSFLCGCRPFGLLDLVT 299
QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSKCMETGYRLAADQHRCEVDVDDCILEPSPCP 319
Db 300 C-ASRNPSSSPCRGGATCVLGP-HGKNYTCRPGYQLDSSQLDCVDVDEC--QDSPCA 355
QY 320 QRCVNTQGGFECHCYNDYLDVGECEVPEVDFPCFRANCEYQCOPLNQTSYLVCVCAEGFAP1 379
Db 356 QECVNTPGGFRCECWGY-----EPGPP-----GEGACQDVDE-----CALGRSP- 395
QY 380 PHEPHRCQMFNCQACPADCDPNTQAS--CECEGYIL--DDGFICTDIDEC--ENGGEFC 433
Db 396 -----CAQGC--TNTDGSFHCSCGEGYVLAGEDGTQCQDVDCVGGGGLC 439
QY 434 SGVCHNLPGTFECICGPDGALVRHIGTDCDSGKV-----DGGDSGSGE-----P 477

Db 440 DSLCFNTQGSFHGCGCLPGWLAPN-GVSCWTMGVSLGPPSGPDEEDKGEKGSTVPRAA 498
QY 478 PPSPTGSGTILTPPA 491
Db 499 TASPTRGPGTTPKA 512

Job time : 43 secs

RESULT 15
US-09-789-919-96
; Sequence 96, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789,919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-789-919-96

Query Match 20.4%; Score 576; DB 9; Length 652;
Best Local Similarity 31.4%; Pred. No. 7e-33;
Matches 174; Conservative 53; Mismatches 201; Indels 126; Gaps 31;
QY 6 QPGSQ-----CUEHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAAD-----VI 53
Db 17 QPGAGTGADTEAVVCGTACTAHSGKLSAAEAQNHCNONGNLTATVKSKEEAQHVRVL 76
QY 54 SLLINGDGGVGR--RLWIGLQLPFG--CGDPKRLGPLRGFWTGTGDNNTSYSRWRLDLN 110
Db 77 AQLRREAALTARMSKFWIGLQREKGLDPSL--PLKGFVWVGGEDETFYSNWHKELRN 134
QY 111 GAPLCGCLVA--VSAEATVPSE--PIWEEQQC-----EVKADGFLCEFFHFPATCRPLA 161
Db 135 SC--ISKRCVSLLLDLSQLLPNLPMWSEGPCSGSPCSNIEGFVCKFSFKGMRPLA 192
QY 162 V-EPGAAAAVSYTYGTPFAARGADFOALPVGSSAAVAPLQLQMC--TAPPGAVQGHW-- 217
Db 193 LGPGP-----QVTTYTPFTTSSLEAVPFASAAVNA-----CGEGDKDETQSHYFL 239
QY 218 -AREAPGAMD-----CSVENGGCEHAC-NAIPGAPRCQCPAGAAALQADGRS 261
Db 240 CKEKAPDVFWSGSGPLCVSPKYGCNPNNGGCHQDCFEFGDGSFLCGCRPRLDLDLVT 299
QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSCMCETGYRLAADQHRCEVDVDDCILEPSPCP 319
Db 300 C-ASRNPCSSSPCKGGATCVLGP-HGKNYTCRCPPQGVQLDSSQLDCVDVDEC--QDSPCA 355
QY 320 QRCVNTQGFECYCHYNYDLVDGCEVVDPCFRANCEYOCQPLNQTSLVCVAEGFAP 379
Db 356 QECVNTPGGRRCWCWGY-----EPGGP-----GEGACQDVDE-----CALGRSP- 395
QY 380 PHEPHRCQFCNQTACPADCPNTOAS--CECPGXYL--DDGFICTDIDEC--ENGGFC 433
Db 396 -----CAQGC-TWIDGSHCSCEGVVLAGEDGTQCCQDVCVPGGGLC 439
QY 434 SGVCHNLPGTFECICGPDLSALVRHIGTDCDSKV-----DGGDSGSGE-----P 477
Db 440 DSLCFNTQGSFHGCGCLPGWLAPN-GVSCWTMGVSLGPPSGPDEEDKGEKGSTVPRAA 498
QY 478 PPSPTGSGTILTPPA 491
Db 499 TASPTRGPGTTPKA 512

Search completed: June 9, 2004, 08:59:53

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:44:08 ; Search time 16.5 Seconds
(without alignments)
2903.235 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516

Perfect score: 2830

Sequence: 1 APAEPQGGQCVEHDCFAL.....PSPTFGSTLTPPAVLVHSG 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2830	100.0	575	1	THHUB
2	1854	65.5	577	2	thrombomodulin pre
3	1092.5	38.6	356	2	thrombomodulin pre
4	416	14.7	1620	2	hypothetical prote
5	414	14.6	1574	2	MEGF6 protein - ra
6	373	13.2	2307	2	fibrillin-2 precu
7	367.5	13.0	1184	2	fibrillin-2 precu
8	367	13.0	2871	2	fibrillin-1 - bovi
9	365	12.9	2918	2	fibrillin-2 precu
10	363	12.8	3002	2	fibrillin-1 precu
11	361	12.8	2871	2	fibrillin-1 precu
12	359	12.7	741	2	hypothetical prote
13	357	12.6	1221	2	fibrillin-2 precu
14	331	11.7	589	2	fibrillin-1D precu
15	329.5	11.6	1964	2	notch4 - mouse
16	327.5	11.6	1712	2	masking protein pr
17	324.5	11.5	689	2	fibrulin, splice fo
18	324.5	11.5	712	2	fibrulin 1, splice
19	320.5	11.3	2321	2	notch3 protein - h
20	320	11.3	1394	2	transforming growt
21	314.5	11.1	3507	2	hypothetical prote
22	313	11.1	601	2	fibrulin 1 precu
23	313	11.1	683	2	fibrulin 1 precu
24	313	11.1	798	2	hypothetical prote
25	312.5	11.0	1820	2	latent transformin
26	308	10.9	685	2	fibrulin, splice fo
27	308	10.9	705	2	fibrulin, splice fo
28	303.5	10.7	1251	2	latent transformin
29	296	10.5	2531	2	notch-1 protein -

ALIGNMENTS

RESULT 1

THHUB

thrombomodulin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence revision 12-May-1995 #text change 15-Sep-2000

C:Accession: A41442; A28307; A29680; A27073; JX0264; S3954

R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyar

J. Biochem. 103, 281-285, 1988

A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed acti

A:Reference number: A41442; MUID:88227301; PMID:2836377

A:Accession: A41442

A:Molecule type: DNA

A:Residues: 1-575 <SHL>

A:Cross-references: DBJ:D00210; NID:G220126; PIDN:BAA00149.1; PID:G220127

R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987

A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cD

A:Reference number: A28307; MUID:87317665; PMID:2819876

A:Accession: A28307

A:Molecule type: DNA; mRNA

A:Residues: 1-472, 'A', 474-575 <JAC>

A:Cross-references: GB:J02973; NID:G339658; PIDN:AAA61175.1; PID:G339659

R:Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioaka, J.; Maruyama, I.; Zushi, M.; Kawah

EMBO J. 6, 1891-1897, 1987

A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endot

A:Reference number: A29680; MUID:88004395; PMID:2820710

A:Accession: A29680

A:Molecule type: mRNA

A:Residues: 1-575 <SUZ>

A:Cross-references: GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G736251

A:Experimental source: lung endothelium

A:Note: Part of this sequence, including the amino end of the mature protein, were dete

R:Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.

Biochemistry 26, 4350-4357, 1987

A:Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of th

A:Reference number: A27073; MUID:88024950; PMID:2822087

A:Accession: A27073

A:Molecule type: mRNA

A:Residues: 1-472, 'A', 474-575 <WEN>

A:Cross-references: GB:M16552; NID:G339656; PIDN:AAB59508.1; PID:G339657

A:Experimental source: placenta

A:Note: parts of this sequence were determined by protein sequencing

R:Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.

J. Biochem. 113, 433-440, 1993

A:Title: Urinary thrombomodulin, its isolation and characterization.

A:Reference number: JX0264; MUID:93293792; PMID:8390446

A:Accession: JX0264

A:Molecule type: protein; mRNA

A:Residues: 19-472, 'A', 474-486 <YAM>

A:Experimental source: urine

A:Note: the urinary form appears to be identical with that circulating in plasma

R:Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.

Biochem. J. 295, 131-140, 1993
 A;Title: Identification of the predominant glycosaminoglycan-attachment site in soluble serine.
 A;Reference number: S38954; MUID:94029900; PMID:8216207
 A;Accession: S38954
 A;Molecule type: protein
 A;Residues: 475-491, 'X', 493-494 <GER>
 A;Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
 R;Meininger, D.P.; Komives, E.A.
 submitted to the Brookhaven Protein Data Bank, September 1995
 A;Reference number: A67369; PDB:1ZQA
 A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 R;Tullinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, August 1994
 A;Reference number: A52804; PDB:1HLT
 A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 submitted to the Brookhaven Protein Data Bank, November 1995
 A;Reference number: A65583; PDB:1FGD
 A;Contents: annotation; conformation by (1)H-NMR, residues 427-444
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 Protein Sci. 5, 195-203, 1996
 A;Title: Structural resiliency of an EGF-like subdomain bound to its target protein, thr
 A;Reference number: A58595; MUID:96276211; PMID:8745396
 A;Contents: annotation; conformation by (1)H-NMR
 C;Genetics:
 A;Gene: GDB:THBD
 A;Cross-references: GDB:119613; OMIM:188040
 A;Map position: 20p11.2-20p11.2
 A;Introns: #status absent
 C;Complex: homodimer, urinary form
 C;Function:
 A;Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
 A;Pathway: blood coagulation moderation
 A;Note: the membrane-bound form is located on the endothelium luminal surface of arterie
 C;Note: thrombin complexed with the membrane-bound form is subject to endocytosis
 C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coag
 e protein
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
 F;19-513/Domain: extracellular #status predicted <EXT>
 F;19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
 F;24-167/Domain: C-type lectin homology <LCH>
 F;177-199/Region: PEST sequence
 F;201-233/Region: PEST sequence
 F;245-280/Domain: EGF homology <EG1>
 F;288-323/Domain: EGF homology <EG2>
 F;329-362/Domain: EGF homology <EG3>
 F;369-404/Domain: EGF homology <EG4>
 F;408-439/Domain: EGF homology <EG5>
 F;445-480/Domain: EGF homology <EG6>
 F;485-513/Region: PEST sequence
 F;517-539/Domain: transmembrane #status predicted <TMN>
 F;540-575/Domain: intracellular #status predicted <INT>
 F;47-115, 116, 382, 403/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;174, 225, 411, 504/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F;245-256, 252-267, 280, 288-296, 292-308, 310-323, 329-340, 336-349, 351-362, 369-378, 374-38
 F;334, 498/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F;490, 492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimen

Query Match 100.0%; Score 2830; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred. No. 9e-165;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPPGSGQCVHEDFCEALYPCGATFLNASQICDGLRGLMTVRSVAADVISLLNGD 60
 Db 19 APAEPPGSGQCVHEDFCEALYPCGATFLNASQICDGLRGLMTVRSVAADVISLLNGD 78
 QY 61 GGVGRRLWIGLQLPPGCGDKPLRGLRQFWVTGNNTSYSRWARLDINGAPLCGLCV 120
 Db 79 GGVGRRLWIGLQLPPGCGDKPLRGLRQFWVTGNNTSYSRWARLDINGAPLCGLCV 138

QY 121 AVSAAEATVPSEPIWBEQCEVKADGFLCEHFHPATCRPLAVEPGAAAAAVSITYGTFFA 180
 Db 139 AVSAAEATVPSEPIWBEQCEVKADGFLCEHFHPATCRPLAVEPGAAAAAVSITYGTFFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGYSQWCETGYRLAA 300
 Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPGSGYSQWCETGYRLAA 318
 QY 301 DQHRCEVDVDCILLEPSPQPCQRCVNTQGGFECHECHYCNVLDVDCVEFPVPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILLEPSPQPCQRCVNTQGGFECHECHYCNVLDVDCVEFPVPCFRANCEYQC 378
 QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQTCACADCDPNTQASCECPGEGVILDDGFI 420
 Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQTCACADCDPNTQASCECPGEGVILDDGFI 438
 QY 421 CTDIDECENGFGCGVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSDSGSGEPPPS 480
 Db 439 CTDIDECENGFGCGVCHNLPGTFECICGPDSSALVRHIGTDCDSKVDGSDSGSGEPPPS 498
 QY 481 PTFGSTLTTPPAVGLVHSG 498
 Db 499 PTFGSTLTTPPAVGLVHSG 516

RESULT 2
 A60501
 thrombomodulin precursor - mouse
 N;Alternate names: fetomodulin
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 16-Jul-1999
 A;Accession: S08488; A32001; A60501
 R;Dittman, W.A.; Majerus, P.W.
 Nucleic Acids Res. 17, 802, 1989
 A;Title: Sequence of a cDNA for mouse thrombomodulin and comparison of the predicted mou
 A;Reference number: S08488; MUID:89128454; PMID:2536925
 A;Accession: S08488
 A;Molecule type: mRNA
 A;Residues: 1-577 <DIT>
 A;Cross-references: EMBL:X14432; NID:gs4781; PID:CAA32597.1; PID:gs4782
 R;Dittman, W.A.; Kumada, T.; Sadler, J.E.; Majerus, P.W.
 J. Biol. Chem. 263, 15915-15922, 1988
 A;Title: The structure and function of mouse thrombomodulin. Phorbol myristate acetate s
 A;Reference number: A32001; MUID:89008498; PMID:2844823
 A;Accession: A32001
 A;Molecule type: mRNA
 A;Residues: 97-577 <DI2>
 A;Cross-references: GB:J04060
 R;Imada, S.; Yamaguchi, H.; Nagumo, M.; Katayanagi, S.; Iwasaki, H.; Imada, M.
 Dev. Biol. 140, 113-122, 1990
 A;Title: Identification of fetomodulin, a surface marker protein of fetal development, a
 A;Reference number: A60501; MUID:90292331; PMID:2162790
 A;Accession: A60501
 A;Molecule type: protein
 A;Residues: 19-22;330-343;479-489;545-555;562-575 <IMA>
 C;Comment: Thrombomodulin binds to and internalizes with thrombin. It is also a cofactor
 C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; membrane protein; phosphoprotein; receptor
 F;24-165/Domain: C-type lectin homology <LCH>
 F;244-279/Domain: EGF homology <EG1>
 F;287-322/Domain: EGF homology <EG2>
 F;328-361/Domain: EGF homology <EG3>
 F;368-403/Domain: EGF homology <EG4>
 F;407-438/Domain: EGF homology <EG5>
 F;444-479/Domain: EGF homology <EG6>

Query Match 65.5%; Score 1854; DB 2; Length 577;
 Best Local Similarity 65.8%; Pred. No. 1.6e-105;

QY	211	GA	VG	QH	W	A	R	E	A	P	G	A	M	D	C	S	V	E	N	G	G	C	H	A	C	N	A	I	P	G	A	P	C	Q	P	A	A	L	Q	A	D	G	R	S	C	T	A	S	Q	S	270						
Db		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
	5	G	T	E	T	G	R	S	R	E	A	P	G	A	C	Q	V	E	R	G	G	Q	H	E	C	K	S	A	G	A	S	N	C	L	C	F	A	D	A	L	Q	A	D	G	R	S	C	G	L	P	A	E	H	P	C	64	
QY	271	N	D	L	C	E	H	F	C	V	P	N	D	P	G	S	C	M	C	E	T	C	Y	R	L	A	A	D	Q	H	R	C	E	D	V	D	C	I	L	E	P	S	P	C	P	C	R	V	N	T	G	G	F	E	330		
Db	65	H	Q	L	C	E	H	F	C	-	-	H	L	G	L	G	N	V	T	C	I	C	E	A	G	Y	Q	L	A	D	H	R	C	E	N	V	D	C	A	Q	L	P	S	P	C	P	C	R	V	N	T	G	G	F	E	122	

MEGF6 protein - rat

```

Query Match      13.2%; Score 373; DB 2; Length 2907;
Best Local Similarity 32.9%; Pred. No. 5e-15;
Matches 102; Conservative 24; Mismatches 92; Indels 92; Gaps 18;

226 DCSVNGGCBHACNAIPGAPPCQAGAAQLQAGRSCTASATQCNLDLCEHFCVNPDP-- 283
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1238 ECMIMNGGCDTQCTNSGSGSYECSCSEGYALMPDRSCA-----DIDE--CENNPDI 1287

284 -----QPGSYSCMCETGYRLAADQHRCEBDVDDCILEPSPCP-ORCVNTQGGFECHCYP 335

```

```

Query Match      13.0%; Score 367.5; DB 2; Length 1184;
Best Local Similarity 30.0%; Pred. No. 5e-15;
Matches 119; Conservative 29; Mismatches 124; Indels 125; Gaps 21;

QY      136 EQQCEVKAD-GFLCEHFHPTC-----RPLAV-----EPGAAAAAVSITYGTFPAARG 183
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      531 EGQSCSENPLGYPCN-HVMLSCEGEPLTPEVRRPEPEAAAPRV-----EAM 582
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      184 ADFOALSVGSSAAV---APLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHCACNA 240
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      583 AGREALSLGTEAELPNSLPGDDQDELLPGEL-----COHLGIN 622
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      241 IPGAPRCQCPAGAAALQADGRSC-----TASAT-----QS 269
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      623 TVGSYHCACPFGLSQDDGRTCRPEGHPQPQEAQEPALKSEFSQVASNTPLPLPQNT 682
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      270 CND--LCEHECVNPDPQFGSYSCMETGYRLAADOHRCEVDVDDCILEPSPCF--QRCVNT 325
Db       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

```

Db 683 CKONGPKQVC---STVGSASCSFPGYAIMADGVSCEDINECVTLDTCSRGEHVNT 739
QY 326 QGQFECH---CYPNYDLVDEGCEVDPDPCFRANCEYQCOPLNQTSLVCV----- 371
Db 740 LGSFHCYKALTCBPGYALKDGECE-EDVDEC--AMGHTTCQP-----GFLCNTKGSFYCOA 792
QY 372 ---CAEGFAFIPH-----EPHRCQMFQNTACPADCDPNTQASCECPGY-I 414
Db 793 RORCMDFLODPEGNCVDINECTSLSEPCRGFSCTINTVGSYTCQNPFLI---CARGYHA 849
QY 415 LDGFTCTDDEGNGGFCSG---VCHNLPTGTECIC 448
Db 850 SDDGAKCVDVNECETVHRCGEGVCHNLPFSYRDC 886

RESULT 8
A55567
fibrillin 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Nov-2003
C:Accession: A55567
R:Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
Genomics 23, 480-485, 1994
A:Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to
A:Reference number: A55567; MUID:95137597; PMID:7835900
A:Accession: A55567
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <TIL>
A:Cross-references: GB:L28748; NID:G508427; PIDN:AAA74122.1; PID:G508428
C:Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 13.0%; Score 367; DB 2; Length 2871;
Best Local Similarity 31.5%; Pred. No. 1.2e-14;
Matches 111; Conservative 26; Mismatches 109; Indels 106; Gaps 20;

QY 226 DCSVNGGCEACNAIPGAPRCQCPAGAAQADGRSTASATQSCNDLCEHFCHVNP--- 282
Db 1200 EGSIMNGGCTCTCTNSGSEYCSQCPGFPALPDQRST-----DIDE--CEDNPNIC 1249
QY 283 -----DQPGSYSCMCETGYRLAADHRCEDVDDCILEPSPC-PQRCVNTQGGFCHVCP 335
Db 1250 DGGQCTNIPGEYRCLCYDGFMASEMDKTCVDNECDLNEINCLSGTCENTKGSFICHDM 1309
QY 336 NYDLVDEG--CVEPVDPC--FRANCEYQCOPLNOT--SYLCVCAEGFA-----PIP 380
Db 1310 GYSGKKGKTGCTD-INECEIGAHCNDRHACVNTAGSFKSCSPGWIGGIKCTDLDECS 1368
QY 381 HEPHRCQMFQNTACPADCDPNTQAS--CECEGYLDDGFTCTDIDE-EN----- 429
Db 1369 NGTHMCSQH-----ADC-KNTMGSYRCLCKEGY-TGDGFTCTDLDESENLNLCNGQ 1419
QY 430 -----GGF-----CS-----GVCHNLPTGTECICGPDSSALV 455
Db 1420 CLNAPGGRRCEDMGFVSADGKACEDIDECSLPNCVFGTCHNLPGLFRCEIGYELD 1479
QY 456 RHIG-----TDCDSGK-VDGSGSGCEPPPTPGSTLTPPAVLV 495
Db 1480 RSGNCTDNECLDPTTCTISGNVNTPGSYTCDCPDD-----FELNPTRVGCV 1527

RESULT 9
A54105
fibrillin-2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 24-Nov-2003
C:Accession: A54105; S17063; S31101
R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguinetti, C.; Bonadio, J.; Mecham, J. Cell Biol. 124, 855-863, 1994
A:Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefe
A:Reference number: A54105; MUID:94165150; PMID:8120105
A:Accession: A54105

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 1-2918 <ZHA>
A:Cross-references: GB:U03272
R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P
Nature 352, 330-334, 1991
A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differ
A:Reference number: S17062; MUID:91304567; PMID:1852206
A:Accession: S17063
A:Molecule type: mRNA
A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>
A:Cross-references: EMBL:X62009
R:Miliewicz, D.M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31101
A:Accession: S31101
A:Molecule type: mRNA
A:Residues: 752-1407, 'R', 1409-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 19
A:Cross-references: EMBL:X62009
C:Genetics:
A:Gene: GDB:FBN2
A:Cross-references: GDB:128122; OMIM:121050
A:Map position: 5q23-5q31
C:Superfamily: fibrillin; EGF homology
C:Keywords: extracellular protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-2918/Product: fibrillin-2 #status predicted <MAT>
F:1245-1280/Domain: EGF homology <EGF1>
F:1970-2013/Domain: EGF homology <EGF>

Query Match 12.9%; Score 365; DB 2; Length 2918;
Best Local Similarity 33.1%; Pred. No. 1.5e-14;
Matches 101; Conservative 25; Mismatches 97; Indels 82; Gaps 17;

QY 226 DCSVNGGCEACNAIPGAPRCQCPAGAAQADGRSTASATQSCNDLCEHFCHVNP--- 283
Db 1244 EGMVNGGCTCTCTNSGSEYCSQCPGFPALPDQRSCA-----DIDE--CENPDTIC 1293
QY 284 -----DQPGSYSCMCETGYRLAADHRCEDVDDCILEPSPC-PQRCVNTQGGFCHVCP 335
Db 1294 DGGQCTNIPGEYRCLCYDGFMASEMDKTCVDNECDLNEINCLSGTCENTKGSFICHQL 1353
QY 336 NYDLVDEG--CVEPVDPC--FRANCEYQCOPLN-OTSILCVCAEGFAFIPH-----EPH 385
Db 1354 GYSVKGKTGCTD-VDECEIGAHCNDRHACVNTAGSFKSCREGW--IGNGIKCIDLDE 1410
QY 386 COMFCNQACPADCDPNTQAS--CECEGYLDDGFTCTDIDE-----CENG----- 430
Db 1411 CSNGTHQCSINAQC-VNTPGSYRCACSEGF-TGDGFTCTDDECAENLNCNGQCLNVP 1468
QY 431 -----GF-----CSGVCHNLPTGTECICGPDSSALVVRHIG- 459
Db 1469 GAYRCECEMGFTPASDSRSCQDIDECSPONICVSGTCNNLPGMFHCICDDGYELDRTOGN 1528
QY 460 -TDCC 463
Db 1529 CTDID 1533

RESULT 10
A47221
fibrillin 1 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 24-Nov-2003
C:Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198
R:Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993
A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain struct
A:Reference number: A47221; MUID:94010947; PMID:7691719
A:Accession: A47221
A:Molecule type: mRNA
A:Residues: 1-337, 'T', 339-1029 <COR>
A:Cross-references: GB:X63556

```

RESULT 12
T46488
hypothetical protein DKFZp434J065.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 04-Feb-2000 #sequence_revision
C.Accession: T46488
04-Feb-2000 #text_change

```

R;Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23035
 A:Accession: T46488
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-741 <AAA>
 A:Cross-references: EMBL:AL337638
 A:Experimental source: adult testis; clone DKFZp434J065
 C:Genetics:
 A:Note: DKFZp434J065.1

Query Match 12.7%; Score 359; DB 2; Length 741;
 Best Local Similarity 31.6%; Pred. No. 1.1e-14;
 Matches 86; Conservative 41; Mismatches 101; Indels 44; Gaps 15;
 QY 227 CSVENGGCEHACNAIPGAPRCQCPAGALQDGRSCTA-SATQSCNDLCEHFCVNPDPQP 285
 DB 68 CAMEHDNCEQLCVNVPQSFVCCQYGVYALAEADGKRCVAVDYCASENHGCHECV-NAD-- 124
 QY 286 GSYSCMCETGYRLAADQHRCEVDVDCILEPSPQRCVNTQGGPECHCYNYDL-VDGEC 344
 DB 125 GSYLCQCEHGFALNPEDEKCTKIDYCASSNHGCOHECVNTDDSYSCHLKGFTLNPDKKT 184
 QY 345 VEPVDPCE--RANCEYQCQPLNQTSLYLCVCAEGFAPIPH-----EPHRCQMFC 390
 DB 185 CRINYLALNKPGEHECVNMEB-SYYCRCHRGYTLDPNGKTCRSVDBHCAQDQHGCEQLC 243
 QY 391 NOTACPADCPNPTQAS--CECPGTYLDDGF-ICTDIDEC--ENGFCGVCCHNUPGTF 444
 DB 244 -----LNTEDSFVCCSGFLNEDLKTCRSVDYCLLSDHG--CHYSCVNMDSRF 291
 QY 445 ECTCGPSALVRHIGTDCDSKVDG---GDSG 473
 DB 292 ACQC-PEGHLVRSDGKTC-AKLDSCALGDHG 320

RESULT 13

A49457
 fibulin-2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-2002
 C:Accession: A49457; S74095
 R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
 J. Cell Biol. 123, 1269-1277, 1993
 A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with
 A:Reference number: A49457; MUID:94064787; PMID:8245130
 A:Accession: A49457
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1221 <PAN>
 A:Cross-references: GB:X75285; NID:9437046; PIDN:CAA53040.1; PID:9437047
 R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 240, 427-434, 1996
 A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases
 A:Reference number: S74094; MUID:96439073; PMID:8841408
 A:Accession: S74095
 A:Molecule type: protein
 A:Residues: 236-238, 'X', 240-247; 260-275; 336-344, 'L', 346-361; 405-426; 566-568, 'EM', 569-589
 C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology
 C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
 F:942-978/Domain: EGF homology <EGF>

Query Match 12.6%; Score 357; DB 2; Length 1221;
 Best Local Similarity 29.5%; Pred. No. 2.2e-14;
 Matches 123; Conservative 39; Mismatches 141; Indels 114; Gaps 27;
 QY 136 BEQCCEVKAD-CFLCEFFHPATC-----RPLAV-----EPGAAAAYS-----IT 174
 DB 521 EQQSCSENFNLGYPNC-HVMLSCCEGEPFLIVPVRPPPEPEAPRRVSEMEMASREALS 579
 QY 175 YGT-----PFAAGADFQ--ALP-----YGSAAVAPLGLQLM-----CTAPPG 211

DB 580 LGTEAEPLNSLPGDDQDECMLPGECLQHLCLINTVSYRCACPFGLQDGRTRCDRGG 639
 QY 212 AVQGHWARE-APGAWDCSV-----ENGGEHACNAIPGAPRCQCPAGAA 254
 DB 640 APQLDTARESAPRSESQAQVSPNTIPLVPQNPCTKNGPCRCQVGVGDTAMCSCFPGYA 699
 QY 255 LQADGRSC-----TASATQSCNDLCEHFCVNPDPQPGSYSC-----MCETGYRLAADQHR 304
 DB 700 IMADGVSCEDQDECLMTHDCS--WKQFCV---NTLGSFYCVNHTVLCAEGYILNA-HRK 753
 QY 305 CEDVDCCILEPSPC--PORCVNTQGGPECH--CYPNYDLVDEGCEVPEVDPCEFA--NC 356
 DB 754 CVVINECVTLHLCTRAEHCVNTGPGFQCYKALTCEPGYVLTGECTD-VDECVTGTGHC 812
 QY 357 E--YQCQPLNQTSLYLCV---CAEGFAPIPH-----EPHRCQMFCNQACPA 397
 DB 813 QAGFSQCN-TKGSFYQARQRCMDGLQDPGEGNCVDINECTSLLEPCRSQFSQINTVGSY 871
 QY 398 DCDPNTQASCECEPGY-ILDDGFICTDIDCEGNGFCSG---VCHNLPGTFECICGP 450
 DB 872 TCORNPLV---CGRGYHANESEGVNBECTGVHRCGEGQLCVNLPGLSGYRCDCKP 925

RESULT 14

T43210
 fibulin-1D precursor - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002
 C:Accession: T43210
 R:Barth, J.L.; Argraves, K.M.; Roark, E.P.; Little, C.D.; Argraves, W.S.
 submitted to the EMBL Data Library, June 1998
 A:Description: Identification of chicken and C. elegans fibulin-1 homologs and character
 A:Reference number: Z22337
 A:Accession: T43210
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-589 <BAR>
 A:Cross-references: EMBL:AF070477; PIDN:AAC24035.1
 C:Genetics:
 A:Note: Intron positions not resolved (incomplete sequence)
 C:Superfamily: fibulin-1; EGF homology

Query Match 11.7%; Score 331; DB 2; Length 589;
 Best Local Similarity 28.1%; Pred. No. 4.6e-13;
 Matches 126; Conservative 49; Mismatches 166; Indels 108; Gaps 28;
 QY 85 GELRGF-QWVTGDNNTSYRWARLDLNGAPLCGLCAVSAEAATVPSPFI-----WEEQ 138
 DB 19 GCLRSFNKCCNGDIETH---ASEIITGEPNDPVLHLGDRCSHCHLCHDRGGEKV 75
 QY 139 QCEVKA-----DGFLECFHFP--ATCRPLAVE-----PGAAAAAVSITYTTPFA--- 180
 DB 76 ECSCRSGFDLAPDGNMACVDHIDECATLMDDCLESQRCCLNTPGSPKIRTLSCGTGYMDS 135
 QY 181 --ARGADFOALPVGSSAAVAPLGLQMLCTAPGAVQ-----GHWAREAPGAWDCS--- 228
 DB 136 ETERCEDVDECNLGH---DCGPLYQCRNTQGSYRCDAKKCGDELONPMTGECTSITC 191
 QY 229 -----VENGGCE-----HACNA-----IPGAPRCQ-----CPAGAAQADGRSCTA 264
 DB 192 PNGYYPKNGMCDIDECVTGHNCGAGECVNTPGFRCCQKGNLCAHYEVN----- 243
 QY 265 SATQSCNDL--CEH-----FCVNPDPQGSYSCMCTGYRLAADQHRCEVDVDCIL--- 313
 DB 244 GATGFCEDVNECQGVCGSMCEI---NLPGYKCKGPGYEFNDKAKKCEVDDECIKAG 300
 QY 314 EFSPCQRCVNTQGGFECHCYPNYDLV-DGCEVPEVDPCEFR--ANCEVQCQPLNQTSLYC 370
 DB 301 HVCDSLAEICINTIGSFCECKKPGQLASDGRRCRCDVNECTTGIAACEQKCVNI-PSGYQC 359
 QY 371 VCAEGFAPIP-----HEPHRCQMFC--NOTACPADCPNPTQAS--CECEPGY-ILDDGFI 420
 DB 360 ICDRGFALGPDGDKCEDIDECISIWAGSGNDLCMGCC--INTKGSYLCQCPGKYIQPDGRT 418

QY 421 CTIDECENGFCG---VCHNLPOTFEC 446
Db 419 CVDVDECMGE-CAGSKVCVNTLGSFKC 446

RESULT 15
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Olin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: EMBL:AF030001; NID:G2564945; PID:G2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>

Query Match 11.6%; Score 329.5; DB 2; Length 1964;
Best Local Similarity 26.3%; Pred. No. 1.6e-12;
Matches 128; Conservative 33; Mismatches 143; Indels 183; Gaps 31;

QY 116 GPLCVAVSAEATVPSEPIWEQCEYKADGFLCE-FHFPAICRPLAVEPGAAAAVSIT 174
Db 35 GGTCLRLSRGGIC-----QC---APGFLGETCQFPDPCR----- 66

QY 175 YGTFPFAARGADFOAL---PVSSAAVAPLGLQLMCTAPPG-----AVQGHWAREAPGAWDC 227
Db 67 -DTQLCKNGSCQALLTPPSRSPTSLTPHFSCPCPSGFTGDRQTHLEELCPSPF-C 124

QY 228 SVENGCGEACNAIPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQG- 286
Db 125 S--NGG-HCYQASGRPQCSCEPGWT-----GEQCO-----LRDFCSANPCANG 166

QY 287 -----SYSCMETGYRLAADHRCF-DVDDCILEPFCPPQ--RCVNTQGGFECCHC--- 333
Db 167 VCLATYPQIQCRCPGF-----EGHTCERDINECFLEFPQCPQTSCHNTLGSYQCLCPVG 222

QY 334 --YPNYDLVDGCEVPVDFCFRANCEYQCOPL---NQTSLVCVARGFAPIPHE----- 382
Db 223 QSGPQCKLRKAGC--PPGSLNGG---TCQLVPEGHSTFHLCLCPPEFTGLDCENMPDC 277

QY 383 -PHRCQMFQNTACADCPDNTQASCECEGYLDGDFICT-DIDCE-----NGGF 432
Db 278 VRHQCO---NGATCLDGLDTYT---CLCPKTW---KGWDCSEDIDECARGPPRCRNGGT 328

QY 433 C-----SGVCHNLPGTFCICGP----- 450
Db 329 QNTAGSFHVCVSGWGGAGCEENLDDCAATCAPGTCIDRVGSFCLCPGRTGLLCH 388

QY 451 --DSALVR--HIGTDCDSKVDG-----GDSGS-----GEPPSP----- 481
Db 389 LEDMCLSQPCHVNAQSTNPLTGLSTLCICQPGYSGSTCHQDLDECQMAQQGSPCEHGS 448

QY 482 ----TFGS 485
Db 449 CINTFGS 455

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:42:38 ; Search time 10.5 Seconds
(without alignments)
2469.613 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516

Perfect score: 2830

Sequence: 1 APAEPQGGQCVHDFAL.....PSPTPGSLTPPAVLVHSG 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2826	99.9	575	1 TRBM_HUMAN	P07204 homo sapien
2	1854	65.5	577	1 TRBM_MOUSE	P15306 mus musculus
3	1092.5	38.6	356	1 TRBM_BOVIN	P06579 bos taurus
4	578	20.4	652	1 CD93_HUMAN	Q9npv3 homo sapien
5	538	19.0	644	1 CD93_MOUSE	O89103 mus musculus
6	521.5	18.4	643	1 CD93_RAT	Q9et61 rattus norv
7	373	13.2	2907	1 FBN2_MOUSE	Q61555 mus musculus
8	367.5	13.0	1184	1 FBL2_HUMAN	P98095 homo sapien
9	367	13.0	2871	1 FBN1_BOVIN	P98133 bos taurus
10	366	12.9	2871	1 FBN1_PIG	Q9tv36 sus scrofa
11	365	12.9	2911	1 FBN2_HUMAN	P35556 homo sapien
12	363	12.8	2871	1 FBN1_HUMAN	P35555 homo sapien
13	361	12.8	2871	1 FBN1_MOUSE	O61554 mus musculus
14	358	12.7	956	1 MTN2_HUMAN	O00339 homo sapien
15	357	12.6	1221	1 FBL2_MOUSE	P37889 mus musculus
16	329.5	11.6	1864	1 NTC3_MOUSE	P31695 mus musculus
17	328.5	11.6	956	1 MTN2_MOUSE	O08746 mus musculus
18	328.5	11.6	1389	1 LTBS_MOUSE	O08746 mus musculus
19	328.5	11.6	1713	1 LTBL_MOUSE	Q8cg18 mus musculus
20	327.5	11.6	1712	1 LTBL_RAT	Q8cg19 mus musculus
21	320.5	11.3	2321	1 NTC3_HUMAN	Q00318 rattus norv
22	320	11.3	1394	1 LTBS_HUMAN	Q9um47 homo sapien
23	320	11.3	1595	1 LTBL_HUMAN	P22064 homo sapien
24	315.5	11.1	443	1 FBL4_HUMAN	Q14766 homo sapien
25	313	11.1	798	1 FBL1_HUMAN	O95967 homo sapien
26	313	11.1	798	1 FBL1_HUMAN	P23142 homo sapien
27	308.5	10.9	443	1 FBL4_CRIGR	O77469 caenorhabdi
28	308.5	10.9	2003	1 NTC3_HUMAN	O55058 cricetus
29	308	10.9	448	1 FBL5_HUMAN	Q9ubx5 homo sapien
30	307	10.8	704	1 FBL1_CHICK	Q73775 gallus gall
31	306.5	10.8	443	1 FBL4_MOUSE	Q9wvj9 mus musculus
32	306	10.8	681	1 FBL1_BRARE	O42182 brachydanio
33	306	10.8	705	1 FBL1_MOUSE	Q08879 mus musculus

RESULT 1

ID	TRBM_HUMAN	STANDARD;	PRT;	575 AA.
AC	P07204;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Thrombomodulin precursor (Fetomodulin) (TM) (CD141 antigen).			
GN	THBD OR THRM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88004395; PubMed=2820710;			
RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioaka J., Maruyama I.,			
RA	Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.,			
RT	"Structure and expression of human thrombomodulin, a thrombin			
RT	receptor on endothelium acting as a cofactor for protein C			
RT	activation."			
RL	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;			
RA	"Human thrombomodulin: complete cDNA sequence and chromosome			
RT	localization of the gene."			
RL	Biochemistry 26:4350-4357(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87317665; PubMed=2819876;			
RA	Jackman R.W., Beeler D.L., Fritze L., Soff G., Rosenberg R.D.;			
RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences			
RT	of the cDNA and gene predict protein structure and suggest sites of			
RT	regulatory control."			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88227901; PubMed=2836377;			
RA	Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.;			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-			
RT	catalyzed activation of protein C."			
RL	J. Biochem. 103:281-285(1988).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			

ALIGNMENTS

ID	TRBM_HUMAN	STANDARD;	PRT;	575 AA.
AC	P07204;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Thrombomodulin precursor (Fetomodulin) (TM) (CD141 antigen).			
GN	THBD OR THRM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88004395; PubMed=2820710;			
RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioaka J., Maruyama I.,			
RA	Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.,			
RT	"Structure and expression of human thrombomodulin, a thrombin			
RT	receptor on endothelium acting as a cofactor for protein C			
RT	activation."			
RL	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;			
RA	"Human thrombomodulin: complete cDNA sequence and chromosome			
RT	localization of the gene."			
RL	Biochemistry 26:4350-4357(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87317665; PubMed=2819876;			
RA	Jackman R.W., Beeler D.L., Fritze L., Soff G., Rosenberg R.D.;			
RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences			
RT	of the cDNA and gene predict protein structure and suggest sites of			
RT	regulatory control."			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88227901; PubMed=2836377;			
RA	Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.;			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-			
RT	catalyzed activation of protein C."			
RL	J. Biochem. 103:281-285(1988).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			

Q9wvh9 mus musculus
Q9wvh8 rattus norv
Q01705 mus musculus
Q9r172 rattus norv
Q35516 mus musculus
Q8nj39 cercopithec
Q12805 homo sapien
Q9w30 rattus norv
Q04721 homo sapien
P46530 brachydanio
P07207 drosophila
Q61982 mus musculus

ID	TRBM_HUMAN	STANDARD;	PRT;	575 AA.
AC	P07204;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
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OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
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RP	SEQUENCE FROM N.A.			
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RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioaka J., Maruyama I.,			
RA	Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.,			
RT	"Structure and expression of human thrombomodulin, a thrombin			
RT	receptor on endothelium acting as a cofactor for protein C			
RT	activation."			
RL	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;			
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RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences			
RT	of the cDNA and gene predict protein structure and suggest sites of			
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RL	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
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RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88227901; PubMed=2836377;			
RA	Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.;			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-			
RT	catalyzed activation of protein C."			
RL	J. Biochem. 103:281-285(1988).			
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RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levenshah M.H., Levenshah M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy D.M., Lovell J.D.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., McMurray A.A.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulton J.B.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20";
RA Nature 414:865-871(2001).
RA [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.S., McSwan P.K., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield F.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [8]
RP CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
RX MEDLINE=94029900; PubMed=8216207;
RA Gerleitz B., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,
RA Grinnell B.W.;
RA "Identification of the predominant glycosaminoglycan-attachment site
RA in soluble recombinant human thrombomodulin: potential regulation of
RA functionality by glycosyltransferase competition for serine474";
RA Biochem. J. 295:131-140(1993).
RA [9]
RP STRUCTURE BY NMR OF 389-407.
RX MEDLINE=96007474; PubMed=7559494;
RA Adler M., Seto M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;
RA "The structure of a 19-residue fragment from the C-loop of the fourth
RA epidermal growth factor-like domain of thrombomodulin";
RA J. Biol. Chem. 270:23366-23372(1995).
RA [10]
RP STRUCTURE BY NMR OF 364-407.
RX MEDLINE=96100636; PubMed=8529067;
RA Meininger D.P., Hunter M.J., Komives E.A.;
RA "Synthesis, activity, and preliminary structure of the fourth
RA EGF-like domain of thrombomodulin";
RA Protein Sci. 4:1683-1695(1995).
RA [11]
RP STRUCTURE BY NMR OF 427-444.
RX MEDLINE=95034791; PubMed=7947766;
RA Srinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
RA "Thrombin-bound structure of an EGF subdomain from human
RA thrombomodulin determined by transferred nuclear Overhauser
RA effects";
RA Biochemistry 33:13553-13560(1994).
RA [12]
RP STRUCTURE BY NMR OF 427-444.
RX MEDLINE=96276211; PubMed=8745396;
RA Hrabal R., Komives E.A., Ni F.;
RA "Structural resiliency of an EGF-like subdomain bound to its target
RA protein, thrombin";
RA Protein Sci. 5:195-203(1996).
RA [13]
RP STRUCTURE BY NMR OF 405-444.
RX MEDLINE=98035729; PubMed=9367781;
RA Sampoli Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;
RA "Structure of the fifth EGF-like domain of thrombomodulin: an
RA EGF-like domain with a novel disulfide-bonding pattern";
RA J. Mol. Biol. 273:913-926(1997).
RA [14]
RP VARIANT TED TYR-486.
RX MEDLINE=95111115; PubMed=7811989;
RA Oehlin A.-K., Marlar R.A.;
RA "The first mutation identified in the thrombomodulin gene in a
RA 45-year-old man presenting with thromboembolic disease";
RA Blood 85:330-336(1995).
RA [15]
RP VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.
RX MEDLINE=97341986; PubMed=9198186;
RA Oehlin A.-K., Norlund L., Marlar R.A.;
RA "Thrombomodulin gene variations and thromboembolic disease";
RA Thromb. Haemost. 78:396-400(1997).
RA [16]
RP VARIANT VAL-473.
RX MEDLINE=97206518; PubMed=9157575;
RA Norlund L., Holm J., Zoller B., Oehlin A.-K.;
RA "A common thrombomodulin amino acid dimorphism is associated with
RA myocardial infarction";
RA Thromb. Haemost. 77:248-251(1997).
RA [17]
RP VARIANT THR-43.
RX MEDLINE=99057299; PubMed=9843165;
RA Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
RA Scubbs P.J., Manger Cats V., Ireland H.;
RA "A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,
RA and the risk of myocardial infarction in men";
RA Thromb. Haemost. 80:743-748(1998).
RA [18]
RP VARIANT VAL-473.
RX MEDLINE=21143723; PubMed=11245641;
RA Wu K.K., Aleksic N., Ahn C., Boerwinkle E., Folsom A.R.,
RA Juneja H.;
RA "Thrombomodulin Ala455Val polymorphism and risk of coronary heart
RA disease";
RA Circulation 103:1386-1389(2001).
RA [19]
RP VARIANT TED TYR-486, AND VARIANT VAL-473.
RX MEDLINE=22135346; PubMed=12139752;
RA Faioni E.M., Franchi F., Castaman G., Biguzzi E., Rodeghiero F.;
RA "Mutations in the thrombomodulin gene are rare in patients with
RA severe thrombophilia";
RA Br. J. Haematol. 118:595-599(2002).
RA CC -!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
RA that forms a 1:1 stoichiometric complex with thrombin. This
RA complex is responsible for the conversion of protein C to the
RA activated protein C (protein Ca). Once evolved, protein Ca
RA scissions the activated cofactors of the coagulation mechanism,
RA factor Va and factor VIIIa, and thereby reduces the amount of
RA thrombin generated.
RA CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
RA CC -!- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
RA thrombomodulin.

[illegible]

```

RESULT 3
TREM_BOVIN
IID TREM_BOVIN STANDARD; PRT; 356 AA.
P06579;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, last sequence update)
16-OCT-2001 (Rel. 40, last annotation update)
Thrombomodulin (Fetomodulin) (TW) (Fragment).
THBD.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
Bovidae; Bovinae; Bos.
NCBI_taxid=9913;
[1]
SEQUENCE FROM N.A.
MEDLINE=87067408; PubMed=3024152;
Jackman R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;
"Characterization of a thrombomodulin cDNA reveals structural
similarity to the low density lipoprotein receptor.";
Proc. Natl. Acad. Sci. U.S.A. 83:8834-8838(1986).
-!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
that forms a 1:1 stoichiometric complex with thrombin. This
complex is responsible for the conversion of protein C to the
activated protein C (protein Ca). Once evolved, protein Ca
scissions the activated cofactors of the coagulation mechanism,
factor Va and factor VIIIa, and thereby reduces the amount of

```

Db 65 HOLCEHFC--HLHGLGNYTCICEAGYQLADQHRCEVDVDCALQPSPCQRCVNTGGFQ 122

Qy 331 CHCYPNVDLVGECVPEVDPCFRANCEYQCOPLNQTSLVLCVCAEGFAPIPHEPHRCQMFC 390

Db 123 CHCTGTVELVDGECVDPVDFDNNCEYQCCPVGRSEHKICACGAFAPVPGAPHKQMFC 182

Qy 391 NOTACPADCPNTQASCECPGEGYILDGFICTDIDCEGNGFCGVCNHLPGTPECICGP 450

Db 183 NOTSCPADCDPHYPTICRCPGEGYIDEGSTCTDINECDT-NICFGQCHNLPSTVEICICGP 241

Qy 451 DSALVRHIGTDCSGKV-----DGDSSGSGPPSPPTGSLTLP-PA-VGLVHSG 498

Db 242 DSALSGQIGIDCDPTQVNEERGTPEDYG--GSGEPVSPVSGATARPSPAPAGLHSG 297

RESULT 4

ID_CD93 HUMAN STANDARD; PRT; 652 AA.

AC QNPY3; Q00274;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Complement component, C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (C1qRp) (C1qRp (p)) (C1q/MBL/SPA receptor) (CD93 antigen) (CDW93).

DE C1QRI OR CD93.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RX MEDLINE=21640567; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leheslahti M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.B., McConachie L.J., McMay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=9719258; PubMed=9047234;

RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;

RT "cDNA cloning and primary structure analysis of C1q(RP), the human C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";

RL Immunity 6:119-129(1997).

RN [2]

RX MEDLINE=21640567; PubMed=11780052;

RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N., Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;

RT "Identification of human CD93 as the phagocytic C1q receptor (C1qRp) by expression cloning.";

RL J. Leukoc. Biol. 71:133-140(2002).

RN [3]

RX MEDLINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leheslahti M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.B., McConachie L.J., McMay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

"The DNA sequence and comparative analysis of human chromosome 20.";

Nature 414:865-871(2001).

[4]

SEQUENCE FROM N.A.

RC TISSUE=Leukocyte;

RX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin I.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RX MEDLINE=21990337; PubMed=11994479;

RA McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.;

RT "Human C1qRp is identical with CD93 and the mmi-11 antigen but does not bind C1q.";

RL J. Immunol. 168:5222-5232(2002).

RN [6]

RX MEDLINE=99192777; PubMed=10092817;

RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;

RT "C1qRp is a heavily O-glycosylated cell surface protein involved in the regulation of phagocytic activity.";

RL J. Immunol. 162:3583-3589(1999).

CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in endothelial cells, platelets, cells of myeloid origin, such as monocytes and neutrophils. Not expressed in cells of lymphoid origin.

CC -!- PTM: N- and O-glycosylated.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 5 EGF-like domains.

CC -!- CAUTION: Has been sometimes referred to as a collectin receptor.

CC -!- CAUTION: According to Ref.5, C1q is not a ligand for C1QRI.

CC -!- DATABASE: NAME=PRO; NOTE=PROW 3.1-6(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/467246456.g.htm".

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CC -----

DR EMBL; U94333; AAB53110.1; --

DR EMBL; AL118508; CAC00597.1; --

DR EMBL; BC028075; AAB28075.1; --

DR HSSP; P35555; IEMN.

DR GENE; HGNC:15855; C1QRI.

DR MIM; 120577; --

DR GO; GO:0016021; C:integral to membrane; IC.

DR GO; GO:0004872; F:receptor activity; NAS.

DR GO:0016337; P:cell-cell adhesion; IDA.
 DR GO:0042116; P:macrophage activation; NAS.
 DR GO:0006909; P:phagocytosis; NAS.
 DR InterPro: IPR00152; Asx hydroxylase.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00008; EGF; 5.
 DR Pfam: PF00059; lectin c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR SMART: SM00179; EGF CA; 3.
 DR PROSITE: PS00010; ASX_HYDROXYL; 3.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS00026; EGF_3; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 652
 FT DOMAIN 24 580
 FT TRANSMEM 581 601
 FT DOMAIN 602 652
 FT DOMAIN 32 174
 FT DOMAIN 260 301
 FT DOMAIN 302 344
 FT DOMAIN 345 384
 FT DOMAIN 385 426
 FT DOMAIN 427 468
 FT DOMAIN 594 601
 FT DISULFID 264 275
 FT DISULFID 271 285
 FT DISULFID 287 300
 FT DISULFID 306 317
 FT DISULFID 311 328
 FT DISULFID 330 343
 FT DISULFID 349 358
 FT DISULFID 354 367
 FT DISULFID 369 383
 FT DISULFID 389 400
 FT DISULFID 396 409
 FT DISULFID 411 425
 FT DISULFID 431 443
 FT DISULFID 439 452
 FT DISULFID 454 467
 FT CARBOHYD 325 325
 FT VARIANT 318 318
 FT
 FT CONFLICT 22 22
 FT CONFLICT 36 36
 FT CONFLICT 38 39
 FT CONFLICT 155 155
 FT CONFLICT 186 186
 FT CONFLICT 492 492
 FT CONFLICT 496 496
 FT CONFLICT 504 504
 FT CONFLICT 541 541
 FT SEQUENCE 652 AA; 68560 MW; EECA0FEAC55FCAC2 CRC64;
 Query Match 20.4%; Score 578; DB 1; Length 652;
 Best Local Similarity 31.6%; Pred. No. 2.7e-31;
 Matches 175; Conservative 52; Mismatches 201; Indels 126; Gaps 31;
 QY 6 QPGSGQ-----CVEHDCFALYFGPATFLNASQICDGLRHLMTVRSSVAAD-----VI 53
 DB 17 QPGAGTGADTEAVCVGTACTYAHSGKLSAARQAQHCNQNGNLATVSKKEAQHVQRVL 76
 QY 54 SILLNGDGVGR--RLWIGLQPLPG-CGDKRLGLRFGVWVTGDNNTSYSRWARLDLN 110
 DB 77 AQLRLREALTARMSKFWIGLQREKGLCDPSL--PLKGFVWVGGEPTFYNWHKELRN 134
 QY 111 GAPLCGPLCVA--VSAAEATVPE-PIWEQQC-----EVKADGFLCEFHFPATCRPLA 161

Db 135 SC--ISKRCVSLLDLSDQLLPRLPKWSEGPCSPGSPGSIENIEGFKFSGKMCPLA 192
 QY 162 V-EPGAAAAVSIITYGTPFAARGADFOALPVGSSAAVAPLGLQLMC-TAPPGAVQGHW-- 217
 Db 193 LGGPG-----QVYITTFPQTSSLEAVPFAAANVA-----CGEGDKDETQSHYFL 239
 QY 218 -AREAPGAWD-----CSVENGGCGHAC-NAIPGAPRCOCAPGAALQADGRS 261
 Db 240 CKEKAPDVEDWSSGSGPLCVSPKYGCNPNNGCGHQDCEGSGDGLCCRCRFRLLDDLV 299
 QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSYCMCTGYRLAADQHRCEVDVDCILEPSPCP 319
 Db 300 C-ASRNPCSSSPCRGGATCVLGP-HGKNYTCRCFQGGYQLDSSLDCCVDVDEC--QSSPCA 355
 QY 320 QRCVNTQGGFECHCYPNYDLVDGCEVPEVDPFCFRANCEYCCQPLNQTSYLCVCAEGFAP 379
 Db 356 QECVNTPGGFRCEWGVY-----EPGGP-----GEGACQDVDE-----CALGRSP- 395
 QY 380 PHEPHRCQMPNQTACPADCDPNTQAS--CECEPGYIL--DDGFICTDIDEC--ENGFC 433
 Db 396 -----CAQGC-TNTDGSFHCSEEGYVLAGEGTQCDVDCVCGPGPLC 439
 QY 434 SGVCHNLPGTFECICGDSALVRHIGTDCDSKV-----DGGDSGSGE-----P 477
 Db 440 DSLCFNTQGSFHCGLPGWVLPN-GVSCVTMGFVSLGPPSPGPDDEBKGEKSGTVPRAA 498
 QY 478 PPSPTPGSTLTTPA 491
 Db 499 TASPTGPGSTPKA 512

RESULT 5
 CD93_MOUSE STANDARD; PRT; 644 AA.
 AC CD93_MOUSE
 AC CD9103;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q
 subcomponent, receptor 1) (ClqR) (ClqR(p)) (Clq/MBL/SPA receptor)
 DE (CD93 antigen) (Cell surface antigen AA4) (Lymphocyte antigen 68).
 GN CLQ1 OR CD93 OR CLQRP OR LY68 OR AA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=20528605; PubMed=11074255;
 RA Kim T.S., Park M., Nepomuceno R.R., Palmirani G., Winokur S.,
 RA Cotman C.A., Bengtsson U., Tenner A.J.;
 RT "Characterization of the murine homolog of ClqR(p): identical cellular
 expression pattern, chromosomal location and functional activity of
 the human and murine ClqR(p).";
 RL Mol. Immunol. 37:377-389(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukemia;
 RX MEDLINE=99330438; PubMed=10403644;
 RA Petrenko O., Beavis A., Klaine M., Kittappa R., Godin I.,
 RA Lemischka I.R.;
 RT "The molecular characterization of the fetal stem cell marker AA4";
 RL Immunity 10:691-700(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv; TISSUE=Endothelial cells, and Spleen;
 RX MEDLINE=99359842; PubMed=10430665;
 RA Norsworthy P.J., Taylor P.R., Walport M.J., Botto M.;
 RT "Cloning of the mouse homolog of the 126-kDa human Clq/MBL/SP-A
 receptor, ClqRp.";
 RL Mamm. Genome 10:789-793(1999).

CC CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for
CC Clq, mannose-binding lectin (MBL2) and pulmonary surfactant
CC protein A (SPA). May mediate the enhancement of phagocytosis in
CC monocytes and macrophages upon interaction with soluble defense
CC collagens. May play a role in intercellular adhesion. Marker for
CC early multipotent hematopoietic precursor cells. May play a role
CC in cell-cell interactions during hematopoietic and vascular
CC development.

CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC CC -!- TISSUE SPECIFICITY: Expressed in lung, heart and bone marrow.
CC Expressed at lower level in ovary, whole embryo and fetal liver.
CC Not detected in brain, adult liver or thymus. Highly expressed in
CC peritoneal cavity and bone marrow macrophages. Not detected in
CC epithelial cells.

CC CC -!- DEVELOPMENTAL STAGE: First detectable in day 9 embryos, in the
CC endocardium and vascular endothelium in the anterior part of the
CC embryo. Expression in endothelial cells, initially restricted to
CC aorta, omphalomesenteric and umbilical arteries, later extends to
CC subcardinal veins, intersegmental arteries and perimeural vessels.
CC On day 10, detectable in the entire embryo.

CC CC -!- PTM: N- and O-glycosylated (By similarity).

CC CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC CC -!- SIMILARITY: Contains 5 EGF-like domains.

CC -----

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CC -----

CC EMBL; AF074856; AAC63274.1; -
CC EMBL; AF081789; AAC62649.1; -
CC EMBL; AF099939; AAD47906.1; -
CC EMBL; AF099938; AAD47906.1; JOINED.
CC HSP; P35555; 1EMN.
CC MGD; MGI:106664; Clqr1.
CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.
CC GO; GO:0016021; C:integral to membrane; ISS.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0004872; F:receptor activity; ISS.
CC GO; GO:0016337; P:cell-cell adhesion; ISS.
CC GO; GO:0042116; P:macrophage activation; ISS.
CC GO; GO:0006909; P:phagocytosis; ISS.
CC InterPro; IPR001152; Asx hydroxyl_s.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR005209; EGF_Like.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00008; EGF; 5.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 3.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE NEG.
CC PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS00026; EGF_3; 4.
CC PROSITE; PS01187; EGF_CA; 3.
CC Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
CC EGF-like domain; Lectin; Glycoprotein.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 644
CC DOMAIN 23 572 COMPLEMENT COMPONENT C1Q RECEPTOR.
CC TRANSMEM 573 593 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 594 644 POTENTIAL.
CC DOMAIN 31 173 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 257 298 C-TYPE LECTIN.
CC DOMAIN 299 341 EGF-LIKE 1.
CC DOMAIN 342 381 EGF-LIKE 2.
CC DOMAIN 382 423 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
CC DOMAIN 424 465 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
CC DISULFID 261 272 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
CC BY SIMILARITY.

FT	DISULFID	268	282	BY SIMILARITY.
FT	DISULFID	284	297	BY SIMILARITY.
FT	DISULFID	303	314	BY SIMILARITY.
FT	DISULFID	308	325	BY SIMILARITY.
FT	DISULFID	327	340	BY SIMILARITY.
FT	DISULFID	346	355	BY SIMILARITY.
FT	DISULFID	351	364	BY SIMILARITY.
FT	DISULFID	366	380	BY SIMILARITY.
FT	DISULFID	386	397	BY SIMILARITY.
FT	DISULFID	393	406	BY SIMILARITY.
FT	DISULFID	408	422	BY SIMILARITY.
FT	DISULFID	428	440	BY SIMILARITY.
FT	DISULFID	436	449	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	CARBOHYD	102	102	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	322	322	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	644 AA;	69354 MW;	EB4351648BF8635A CRC64;

Query Match 19.0%; Score 538; DB 1; Length 644;
Best Local Similarity 29.9%; Pred. No. 1.2e-28;
Matches 159; Conservative 53; Mismatches 200; Indels 120; Gaps 25;

QY	12	CVEHDFALYPCGPATFLNASQICDGLRGHLMTVRSVAA	-----DVISLLNGDGGVGR--	66
Db	30	CEGTACYTAHWGKLSAAEQHRCNENGNGNLATVSEEARHVQQAQTLLKTKAPLEAKM	-----RVVTYT	89
QY	67	RLWTGLQLPFGCGDKPLRGFWVTGDNNTSYSRWARLDLNGAPLCGPLCAVSA	-----	125
Db	90	GKFWIGLQREKNGNCTYHDL-PWRGFSWVGGEDEYASWYKASKSCITPKRCVSLDLS	-----	148
QY	126	EATVPSK-PIVEEQCEV-----KADGFLCEHFPATCRFLAV-EPGAAAAAIVTGT	-----GAW	225
Db	149	LTPHPSHLPKWHESPCGTPEAPGNSIEGFLCKFNPKMCRDLALGGPG-----	-----RVVTYT	202
QY	178	PFAARGADFOALPVGSSAAVAPLGIQ-----LMCT-APGAVQGHAREAP-----	-----GAW	225
Db	203	PFQATTSLEAVPPASVANVA-CGDEAKSETHYFLCNKTEGIF--HWGSSGGLCVSPKF	-----	259
QY	226	DCSVENGCGEHAC-NAIPGAPRCQCPAGAAQADGRSCTASATQSCNDLCBHFCVNPNDQ	-----	284
Db	260	GCSEFNGGCGQDCPEGGDGSFRCRPGFRLDLLVTAS-----RNPSSNPT	-----	309
QY	285	PG-----SYSCMCTGYRLAAQHRCEVDVDDCILESPSPQPCRVNTGGFECY	-----	334
Db	310	GGGMCHSVPLSENYTCRCPGYQLDSSQVHCVDIDEC--QDSPAQCDCVNTLGSFHCW	-----	367
QY	335	PNYDLVDG---ECVEPVDPFRANCEYQCQLNNTSVLCVCAEGFAPIPHPHRCQMFN	-----	391
Db	368	VGIQ-PSGPKKEACEDVDECAANSF-----CAQGC	-----	398
QY	392	QTACPADCDPNTQAS--CECPGYIL--DDGFICTIDECEN--GGFCSGVCHNLPGTFE	-----	445
Db	399	-----NTDGSFYCSCKEYIVSGEDSTQCEDIDECSDARGNFCDSLCTNTDGSFR	-----	448
QY	446	CICGPDLSALVRHIGTDCDSG-----KVDGDSGSGBPPTPGS	-----	485
Db	449	CGCPFGWELAPN-GVFCRGTVFSELPARPQKEDNDNRKSTMPPTMPSTP	-----	499

RESULT 6
CD93_RAT
ID CD93_RAT STANDARD; PRT; 643 AA.
AC Q9ET61; Q9JIZ6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement component C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (Clqrp) (Clqr(p)) (Clq/MBL/SPA receptor) (CD93 antigen) (Cell surface antigen AA4).
GN C1QR1 OR CD93 OR C1QRP.
OS Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PVG; TISSUE=Natural killer cells;
 RX MEDLINE=20545218; PubMed=11093152;
 RA Lovik G., Vaage J.F., Dissen E., Spierer C., Ryan J.C., Rolstad B.;
 RT "Characterization and molecular cloning of rat C1qR, a receptor on NK
 cells.";
 RL Eur. J. Immunol. 30:3355-3362(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wislar; TISSUE=Lung;
 RX MEDLINE=20507883; PubMed=10334210;
 RA Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;
 RT "Molecular and cellular properties of the rat AA4 antigen, a C-type
 lectin-like receptor with structural homology to thrombomodulin.";
 RL J. Biol. Chem. 275:34382-34392(2000).
 CC -|- FUNCTION: Receptor (or element of a larger receptor complex) for
 C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
 protein A (SPA). May mediate the enhancement of phagocytosis in
 monocytes and macrophages upon interaction with soluble defense
 collagens. May play a role in intercellular adhesion.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and
 heart. Expressed at lower level in brain, thymus, liver, spleen,
 intestine, kidney, adrenal gland, muscle and testis. Expressed on
 endothelial cells, platelets, undifferentiated monocytes and
 circulating natural killer cells.
 CC -|- PTM: N- and O-glycosylated (By similarity).
 CC -|- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -|- SIMILARITY: Contains 5 EGF-like domains.
 CC
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 CC
 DR EMBL; AF136537; AAG01572.1; -;
 DR EMBL; AF160978; AAF80402.1; -;
 DR HSP; P35555; IEMN
 DR GO; GO:0016021; C: integral to membrane; ISS.
 DR GO; GO:0004872; F: receptor activity; ISS.
 DR GO; GO:0016337; P: cell-cell adhesion; ISS.
 DR GO; GO:0042116; P: macrophage activation; ISS.
 DR GO; GO:0006909; P: phagocytosis; ISS.
 DR InterPro; IPR000152; Asx hydroxylase.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein.
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DB 1518 RTGGNCTDID 1527

RESULT 8

ID	FBL2_HUMAN	STANDARD;	PRT; 1184 AA.
AC	P98035;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Fibulin-2 precursor.		
GN	FBLN2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Fibroblast;		
RC	MEDLINE=95104855; PubMed=7806230;		
RX	Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,		
RA	Chu M.-L.;		
RA	"Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping		
RT	of the gene on human and mouse chromosomes.";		
RT	Genomics 22:425-430(1994).		
RL	[2]		
RP	DEVELOPMENTAL STAGE.		
RX	MEDLINE=96301678; PubMed=8737292;		
RA	Miesege N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;		
RT	"The extracellular matrix proteins fibulin-1 and fibulin-2 in the		
RT	early human embryo.";		
RL	Histochem. J. 28:109-116(1996).		
CC	-!- FUNCTION: Its binding to fibronectin and some other ligands is		
CC	calcium dependent.		
CC	-!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By		
CC	similarity).		
CC	-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.		
CC	-!- TISSUE SPECIFICITY: Component of both basement membranes and other		
CC	connective tissues. Expressed in heart, placenta and ovary.		
CC	-!- DEVELOPMENTAL STAGE: Widely expressed during embryonic		
CC	development. Primarily detected within the neuroepithelium, spinal		
CC	ganglia and peripheral nerves.		
CC	-!- SIMILARITY: Belongs to the fibulin family.		
CC	-!- SIMILARITY: Contains 3 anaphylatoxin-like domains.		
CC	-!- SIMILARITY: Contains 11 EGF-like domains.		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
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CC	or send an email to license@isb-sib.ch).		
CC			
DR	EWBL; X82494; CAA57876.1; --		
DR	PIR; A55184; A55184.		
DR	HSSP; P00736; IAPQ.		
DR	Genew; HGNC:3601; FBLN2.		
DR	MTM; 135821; --		
DR	GO; GO:0005578; C:extracellular matrix; TAS.		
DR	GO; GO:0005509; F:calcium ion binding; TAS.		
DR	GO; GO:0005201; F:extracellular matrix structural constituent; TAS.		
DR	InterPro; IPR000020; Anaphylatoxin		
DR	InterPro; IPR000152; Asx_hydroxyl_S.		
DR	InterPro; IPR001881; EGF_CA.		
DR	InterPro; IPR006209; EGF_like.		
DR	Pfam; PF01821; ANATO; 2.		
DR	Pfam; PF00008; EGF; 5.		
DR	SMART; SM00104; ANATO; 3.		
DR	SMART; SM00179; EGF_CA; 9.		
DR	PROSITE; PS01177; ANAPHYLATOXIN 1; 3.		
DR	PROSITE; PS01178; ANAPHYLATOXIN 2; 3.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 5.		

DR PROSITE; PS00022; EGF 1; FALSE_NEG.
 DR PROSITE; PS01386; EGF 2; 5.
 DR PROSITE; PS00026; EGF 3; 4.
 DR PROSITE; PS01187; EGF CA; 9.
 KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 KW Calcium-binding; Repeat.
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 FT SEQUENCE 1184 AA; 126543 MW; CA48490A5F9EC5D CRC64;
 Query Match 13.0%; Score 367.5; DB 1; Length 1184;
 Best Local Similarity 30.0%; Pred. No. 4.1e-17;
 Matches 119; Conservative 29; Mismatches 124; Indels 125; Gaps 21;
 QY 136 EEQQCEVKAD-GFLCEHFPATC-----RPLAV-----EPGAAAASVITYGTFPAARG 183

Db 531 EQGSCSNPILGYPNCN-HVMLSCCEGEEPLIPEVRPRPEPAAAPRRVS-----EAM 582
 QY 184 ADFQALPVGGSAAV---APLGLQLMCTAPPGAVQGHWAREAPGAWDCSVEGGCBHACNA 240
 Db 583 AGREALSLGTEAEPLNSLFGDDQDECLLLPGEL-----CQLLCIN 622
 QY 241 IPGAPROCPCAGALQADGRSC-----TASAT-----QS 269
 Db 623 TVGSYHCAFCFGFSQLDDGRTCPREGHPQPEAQEPALKSEFQVAVNTIPLPQNT 682
 QY 270 CND--LCEHFCVPNDQGSYCMCTGYRLAAQHCEDVDDCILESPCP--QRCVNT 325
 Db 683 CKNGPKQVC---STVGSAICSCFFGYAIMADGVSCEDINECVTDLHTCSRGEHCVT 739
 QY 326 QGSEFCH---CYPNYDLVDGECVPEVDPCFRANCEYQCQPLNQTSLVCV----- 371
 Db 740 LGSFHYKALTCEPGYALKGEC-EDVDEC--AMGTHTCQP-----GFLQNTKGSFYCQA 792
 QY 372 ---CAEGFAPIPH-----EPHRCQMFNCNOTACPADCDPNTQASCECEGY-I 414
 Db 793 RQRCMDGFLQDPGNGCVDINECTSLSPCRPGFSCINTVGSYTCORPLI---CARGYHA 849
 QY 415 LDGFICTDIDECENGQFCSG---VCHNLPGETPECIC 448
 Db 850 SDGAKCDVNECETGVHRCGEGQVCHNLPFSYRDC 886

RESULT 9
 FBNI_BOVIN
 ID FBNI_BOVIN STANDARD; PRT; 2871 AA.
 AC P98133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor (MF340).
 GN FBNI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=95137597; PubMed=7835900;
 RA Tilstra D.J., Potter K.A., Byers P.H.;
 RT "Sequence of the coding region of the bovine fibrillin cDNA and
 RT localization to bovine chromosome 10.";
 RL Genomics 23:480-485(1994).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=96132851; PubMed=8557636;
 RA Gibson M.A., Hatzinikolas G., Kumaratilake J.S., Sandberg L.B.,
 RA Nicholl J.K., Sutherland G.R., Cleary E.G.;
 RT "Further characterization of proteins associated with elastic fiber
 RT microfibrils including the molecular cloning of MAGP-2 (MP25).";
 RL J. Biol. Chem. 271:1096-1103(1996).
 CC -!- FUNCTION: Structural component of connective tissue microfibrils
 CC that binds calcium. Fibrillin-1-containing microfibrils provide
 CC long-term force bearing structural support.
 CC -!- PTM: Forms intermolecular disulfide bonds either with other
 CC fibrillin-1 molecules or with other components of the
 CC microfibrils.
 CC -!- SIMILARITY: Contains 47 EGF-like domains.
 CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBRP) domains.
 CC -----
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CC CC ENBL; L28748; AAA74122.1; -

DR DR PIR; A55567; A55567.

DR DR HSP; P35555; IAPJ.

DR DR InterPro; IPR000152; Asx hydroxyl_s.

DR DR InterPro; IPR001881; EGF_Ca.

DR DR InterPro; IPR006205; EGF-like.

DR DR InterPro; IPR002212; Fibril-assoc.

DR DR Pfam; PF00008; EGF; 46.

DR DR Pfam; PF00683; TB; 9.

DR DR SMART; SM00179; EGF_Ca; 42.

DR DR PROSITE; PS00010; ASX HYDROXYL; 43.

DR DR PROSITE; PS00022; EGF_1; 2.

DR DR PROSITE; PS01186; EGF_2; 38.

DR DR PROSITE; PS00026; EGF_3; 45.

DR DR PROSITE; PS01187; EGF_Ca; 43.

KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;

KW Repeat; Signal; Multigene family;

FT SIGNAL 1 27 POTENTIAL.

FT CHAIN 28 2871 FIBRILLIN 1.

FT DOMAIN 81 112 EGF-LIKE 1.

FT DOMAIN 115 146 EGF-LIKE 2.

FT DOMAIN 147 178 EGF-LIKE 3.

FT DOMAIN 246 287 EGF-LIKE 4.

FT DOMAIN 288 329 EGF-LIKE 5.

FT REPEAT 330 390 TGFBP 1.

FT DOMAIN 392 446 PRO-RICH.

FT DOMAIN 449 489 EGF-LIKE 6.

FT DOMAIN 490 529 EGF-LIKE 7.

FT DOMAIN 530 571 EGF-LIKE 8.

FT DOMAIN 572 612 EGF-LIKE 9.

FT DOMAIN 613 653 EGF-LIKE 10.

FT REPEAT 654 722 TGFBP 2.

FT DOMAIN 723 764 EGF-LIKE 11.

FT DOMAIN 765 806 EGF-LIKE 12.

FT DOMAIN 807 846 EGF-LIKE 13.

FT DOMAIN 910 951 EGF-LIKE 14.

FT REPEAT 952 1027 TGFBP 3.

FT DOMAIN 1028 1069 EGF-LIKE 15.

FT DOMAIN 1070 1112 EGF-LIKE 16.

FT DOMAIN 1113 1154 EGF-LIKE 17.

FT DOMAIN 1155 1196 EGF-LIKE 18.

FT DOMAIN 1197 1237 EGF-LIKE 19.

FT DOMAIN 1238 1279 EGF-LIKE 20.

FT DOMAIN 1280 1321 EGF-LIKE 21.

FT DOMAIN 1322 1362 EGF-LIKE 22.

FT DOMAIN 1363 1403 EGF-LIKE 23.

FT DOMAIN 1404 1445 EGF-LIKE 24.

FT DOMAIN 1446 1486 EGF-LIKE 25.

FT DOMAIN 1487 1527 EGF-LIKE 26.

FT REPEAT 1528 1605 TGFBP 4.

FT DOMAIN 1606 1647 EGF-LIKE 27.

FT DOMAIN 1648 1688 EGF-LIKE 28.

FT REPEAT 1689 1765 TGFBP 5.

FT DOMAIN 1766 1807 EGF-LIKE 29.

FT DOMAIN 1808 1848 EGF-LIKE 30.

FT DOMAIN 1849 1890 EGF-LIKE 31.

FT DOMAIN 1891 1929 EGF-LIKE 32.

FT DOMAIN 1930 1972 EGF-LIKE 33.

FT DOMAIN 1973 2012 EGF-LIKE 34.

FT DOMAIN 2013 2054 EGF-LIKE 35.

FT REPEAT 2055 2126 TGFBP 6.

FT DOMAIN 2127 2165 EGF-LIKE 36.

FT DOMAIN 2166 2205 EGF-LIKE 37.

FT DOMAIN 2206 2246 EGF-LIKE 38.

FT DOMAIN 2247 2290 EGF-LIKE 39.

FT DOMAIN 2291 2332 EGF-LIKE 40.

FT REPEAT 2333 2401 TGFBP 7.

FT DOMAIN 2402 2443 EGF-LIKE 41.

FT DOMAIN 2444 2484 EGF-LIKE 42.

FT DOMAIN 2485 2523 EGF-LIKE 43.

FT DOMAIN 2524 2566 EGF-LIKE 44.

FT DOMAIN 2567 2607 EGF-LIKE 45.

FT DOMAIN 2607 2647 EGF-LIKE 46.

FT DOMAIN 2648 2687 EGF-LIKE 47.

FT DISULFID 85 94 BY SIMILARITY.

FT DISULFID 89 100 BY SIMILARITY.

FT DISULFID 102 111 BY SIMILARITY.

FT DISULFID 119 129 BY SIMILARITY.

FT DISULFID 123 134 BY SIMILARITY.

FT DISULFID 136 145 BY SIMILARITY.

FT DISULFID 150 160 BY SIMILARITY.

FT DISULFID 154 166 BY SIMILARITY.

FT DISULFID 168 177 BY SIMILARITY.

FT DISULFID 250 262 BY SIMILARITY.

FT DISULFID 257 271 BY SIMILARITY.

FT DISULFID 273 286 BY SIMILARITY.

FT DISULFID 292 304 BY SIMILARITY.

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FT DISULFID 433 465 BY SIMILARITY.

FT DISULFID 460 474 BY SIMILARITY.

FT DISULFID 476 488 BY SIMILARITY.

FT DISULFID 494 504 BY SIMILARITY.

FT DISULFID 499 513 BY SIMILARITY.

FT DISULFID 515 528 BY SIMILARITY.

FT DISULFID 534 546 BY SIMILARITY.

FT DISULFID 541 555 BY SIMILARITY.

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FT DISULFID 576 587 BY SIMILARITY.

FT DISULFID 582 596 BY SIMILARITY.

FT DISULFID 598 611 BY SIMILARITY.

FT DISULFID 617 628 BY SIMILARITY.

FT DISULFID 623 637 BY SIMILARITY.

FT DISULFID 639 652 BY SIMILARITY.

FT DISULFID 727 739 BY SIMILARITY.

FT DISULFID 734 748 BY SIMILARITY.

FT DISULFID 750 763 BY SIMILARITY.

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FT DISULFID 776 790 BY SIMILARITY.

FT DISULFID 792 805 BY SIMILARITY.

FT DISULFID 811 821 BY SIMILARITY.

FT DISULFID 816 830 BY SIMILARITY.

FT DISULFID 832 845 BY SIMILARITY.

FT DISULFID 914 926 BY SIMILARITY.

FT DISULFID 921 935 BY SIMILARITY.

FT DISULFID 937 950 BY SIMILARITY.

FT DISULFID 1032 1044 BY SIMILARITY.

FT DISULFID 1039 1053 BY SIMILARITY.

FT DISULFID 1055 1068 BY SIMILARITY.

FT DISULFID 1074 1085 BY SIMILARITY.

FT DISULFID 1081 1095 BY SIMILARITY.

FT DISULFID 1097 1111 BY SIMILARITY.

FT DISULFID 1117 1129 BY SIMILARITY.

FT DISULFID 1124 1138 BY SIMILARITY.

FT DISULFID 1140 1153 BY SIMILARITY.

FT DISULFID 1159 1171 BY SIMILARITY.

FT DISULFID 1166 1180 BY SIMILARITY.

FT DISULFID 1182 1195 BY SIMILARITY.

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FT DISULFID 1208 1221 BY SIMILARITY.

FT DISULFID 1223 1236 BY SIMILARITY.

FT DISULFID 1242 1254 BY SIMILARITY.

FT DISULFID 1249 1263 BY SIMILARITY.

FT DISULFID 1265 1278 BY SIMILARITY.

FT DISULFID 1284 1296 BY SIMILARITY.

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FT DISULFID 1307 1320 BY SIMILARITY.

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 FT DISULFID 1513 1526 BY SIMILARITY.
 FT DISULFID 1610 1622 BY SIMILARITY.
 FT DISULFID 1617 1631 BY SIMILARITY.
 FT DISULFID 1633 1646 BY SIMILARITY.

Query Match
 Best Local Similarity 13.0%; Score 367; DB 1; Length 2871;
 Matches 111; Conservative 26; Mismatches 109; Indels 106; Gaps 20;

QY 226 DCSVNGGACNAIPGAPROCPAGALQADGSCSTASATQSCNDLCEHFCVNP---282
 :||:|||||
 Db 1200 ECSINMGCTCTNSEGSGYSCQPGFALPDQSCCT-----DIDE--CEDNPNC 1249
 :||:|||||

QY 283 -----DQPSYSCMCETGYRLAADQRCEDVDCCILEPSPC-PQRCVNTQGGFCHCVP 335
 :||:|||||
 Db 1250 DGGQCTNIPGEYRCLCYDGFMASEDMDKTCVDVNECDLNPICLCTGCTKSGFICHDM 1309
 :||:|||||

QY 336 NYDLVDGE--CVERVDPG--FRANCEYOCQPLNQT-SYLCVCAEFGA-----PIP 380
 :||:|||||

Db 1310 GYSGKKGKTGCTD-INECEIGHNCDRHAVCTNTAGSFKCSGPGWIGDKICTDLDECS 1368
 :||:|||||

QY 391 HEPHRCQMPNQTACPADCDPNTQAS--CECEGYILDGFTCTDIDSC-EN-----429
 :||:|||||

Db 1369 NGTHMCSQH-----ADC-KNTMGSYRCLCKEYI-TGDGFTCTDLDECSNMLCGNGQ 1419
 :||:|||||

QY 430 -----GGF-----CS-----GVCHNLPGTFECIGPDSALV 455
 :||:|||||

Db 1420 CLNAPGYRCEDMGFVPSADGKACEDIDCSLNPICVFGTCHNLPLGLFRCEIGYELD 1479
 :||:|||||

QY 456 RHIG-----TDCDSK-VDGDGSGGEPSPPTPGSTTTPPAVLV 495
 :||:|||||

Db 1480 RSGNCTDVNECLDPTTCISGNVNTPGSYTCDPCPD-----FELNTRVGV 1527
 :||:|||||

RESULT 10
 ID FBNI_PIG STANDARD; PRT: 2871 AA.
 AC Q9TV36;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBNI.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=99156858; PubMed=10036187;
 RA Biery N.J., Eladad Z.A., Moore C.S., Stetten G., Spencer F.,
 RA Dietz H.C.;
 RT "Revised genomic organization of FBNI and significance for regulated
 RL gene expression.";
 RL Genomics 56:70-77(1999).
 CC -!- FUNCTION: Structural component of connective tissue microfibrils
 CC that binds calcium. Fibrillin-1-containing microfibrils provide
 CC long-term force bearing structural support.
 CC -!- PTM: Forms intermolecular disulfide bonds either with other
 CC fibrillin-1 molecules or with other components of the
 CC microfibrils.
 CC -!- SIMILARITY: Contains 47 EGF-like domains.
 CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
 CC -----
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DR EMBL; AF073800; AAD50328.1; -
 DR HSSP; P35555; IAPU.
 DR InterPro; IPR00152; Asx hydroxyl_s.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002212; Fibrin-assoc.
 DR Pfam; PF00008; EGF; 44.
 DR Pfam; PF00683; TB; 9.
 DR SMART; SM00179; EGF_CA; 40.
 DR PROSITE; PS00010; ASX HYDROXYL; 41.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 36.
 DR PROSITE; PS00026; EGF_3; 43.
 DR PROSITE; PS01187; EGF_CA; 41.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family
 FT SIGNAL 1 27
 FT CHAIN 28 2871
 FT FIBRILLIN 1.
 FT EGF-LIKE 1.
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FT DOMAIN 2648 2687 EGF-LIKE 47, CALCIUM-BINDING.
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Query Match 12.9%; Score 366; DB 1; Length 2871;
Best Local Similarity 30.6%; Pred. No. 1.2e-16;
Matches 109; Conservative 26; Mismatches 107; Indels 114; Gaps 20;
QY 226 DCSVNGGSGHACNAIPGAPRCQCPAGAAQADGRSTASATQSCNDLCEHFCVNP--- 282
DB 1200 ECSIMNGGCEFTCTNSEGSEYSCQPGFALPMDQSRCT-----DIDE--CEDNPNIC 1249
QY 283 -----DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSC-PORCVNTQGGFECHCYP 335
DB 1250 DGGQCTNIPEYRCLCYDGFWASEDMKTCVDVNECDLNPICLSGTCENTKGSFICHCDM 1309
QY 336 NYDLVDGE--CPEPVDPC--FRANCEYQCOFLNQT-SYLCVCAEGFA-----PIP 380
DB 1310 GYSGKKGKGTCTD-INECEIGAHCNDRHAVCTNTAGSFNCSCSPGWIQDKICTDLDECS 1368
QY 381 HEHRCQMFQNTACPADCDPNTQAS--CECPGYILDDGFICTDIDEC-EN----- 429
DB 1369 NGTHMCSQH-----ADC-KNTMGSYRLCKEGY-TGDGFTCADLDECSNVKLCGNVQ 1419
QY 430 -----GGF-----CS-----GVCHNLPGTFECICGPDALV 455
DB 1420 CLYAPGGYHCEYDGMGFVPSADRSKSCVDSDECSLPNCTCVFTCHNLPLFCFCB----- 1472
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RESULT 11
FBN2 HUMAN
ID FBN2 HUMAN STANDARD; PRT; 2911 AA.
AC P35556;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrillin 2 precursor.
GN FBN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94165150; PubMed=8120105;
RA Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguineti C.,
RA Bonadio J., Meham R.P., Ramirez F.
RT "Structure and expression of fibrillin-2, a novel microfibrillar
```

RT component preferentially located in elastic matrices.";

RL J. Cell Biol. 124:855-863(1994).

RN [2]

RP SEQUENCE OF 752-1505 FROM N.A.

RX MEDLINE=91304567; PubMed=1852206;

RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,

RT Tsiouras P., Ramirez F., Hollister D.;

RT "Linkage of Marfan syndrome and a phenotypically related disorder to

RT two different fibrillin genes.";

RL Nature 352:330-334(1991).

RN [3]

RP VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILB-964.

RX MEDLINE=96083599; PubMed=7493032;

RA Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;

RT "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,

RT congenital contractual arachnodactyly.";

RL Nat. Genet. 11:456-458(1995).

RN [4]

RP VARIANTS CCA HIS-1114.

RX MEDLINE=98407789; PubMed=9737771;

RA Babcock D., Gasner C., Francke U., Maalen C.;

RT "A single mutation that results in an asp-to-his substitution and

RT partial exon skipping in a family with congenital contractual

RT arachnodactyly.";

RL Hum. Genet. 103:22-28(1998).

RN [5]

RP VARIANTS CCA PHE-1141 AND TRP-1252.

RX MEDLINE=20259236; PubMed=10797416;

RA Belleh S., Zhou G., Wang M., Der Kaloustian V.M., Pagon R.A.,

RT Godfrey M.;

RT "Two novel fibrillin-2 mutations in congenital contractual

RT arachnodactyly.";

RL Am. J. Med. Genet. 92:7-12(2000).

CC -!- FUNCTION: Structural component of connective tissue microfibrils

CC that binds calcium. Fibrillin-2-containing microfibrils regulate

CC the early process of elastic fiber assembly.

CC -!- DISEASE: Defects in FBN2 are the cause of congenital contractual

CC arachnodactyly (CCA) [MIM:121050]; also known as Beals syndrome.

CC CCA is phenotypically similar to Marfan syndrome, but does not

CC effect the aorta and the eyes.

CC -!- SIMILARITY: Contains 47 EGF-like domains.

CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.

CC -!- DATABASE: NAME=Elastic Fiber Homepage; NOTE=Fibrillin 2 page;

CC WWW="http://ef.wustl.edu/genes/FBN2.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

DR ENBL; U03272; AAA18950.1; -.

DR ENBL; X62009; -; NOT_ANNOTATED_CDS.

DR PIR; A54105; A54105.

DR HSSP; P35555; 1EMN.

DR Genew; HGNC:3604; FBN2.

DR MIM; 121050; -.

DR GO; GO:0005578; C:extracellular matrix; TAS.

DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002212; Fibril-assoc.

DR Pfam; PF000683; TB_9.

DR PRINTS; PR00010; EGFBL00D.

DR SMART; SM00179; EGF_CA; 43.

DR PROSITE; PS00010; ASX_HYDROXYL; 43.

DR PROSITE; PS00022; EGF_1; 2.

DR PROSITE; PS01186; EGF_2; 37.

DR PROSITE; PS00026; EGF_3; 45.

DR PROSITE; PS01187; EGF_CA; 42.

KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;

KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.

FT SIGNAL 1 28

FT CHAIN 29 2911

FT DOMAIN 111 142

FT EGF-LIKE 1. 142

FT DOMAIN 145 176

FT EGF-LIKE 2. 176

FT DOMAIN 176 207

FT EGF-LIKE 3. 207

FT DOMAIN 275 316

FT EGF-LIKE 4. 316

FT REPEAT 317 358

FT EGF-LIKE 5. 358

FT DOMAIN 359 425

FT EGF-LIKE 6. 425

FT DOMAIN 493 533

FT EGF-LIKE 7. 533

FT DOMAIN 534 573

FT EGF-LIKE 8. 573

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FT EGF-LIKE 9. 615

FT DOMAIN 616 656

FT EGF-LIKE 10. 656

FT REPEAT 657 697

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FT EGF-LIKE 12. 766

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FT EGF-LIKE 13. 808

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FT EGF-LIKE 14. 850

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FT EGF-LIKE 15. 890

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FT DOMAIN 1199 1240

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FT DOMAIN 1891 1932

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FT EGF-LIKE 55. 2733

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FT DISULFID 153 164

FT DISULFID 166 175

FT DISULFID 180 190

FT DISULFID 184 195

FT DISULFID 197 206

FT DISULFID 279 291

FT DISULFID 286 300

"Software and database for the analysis of mutations in the human FBN1 gene.",
 RT Nucleic Acids Res. 24:137-141(1996).
 RN [10]
 RP REVIEW ON MFS VARIANTS.
 RX MEDLINE=97169383; PubMed=9016526;
 RA Collod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
 RA Richards R.I., Wang W., Junien C., Boileau C.;
 RT Marfan Database (second edition): software and database for the
 RT analysis of mutations in the human FBN1 gene.;
 RN Nucleic Acids Res. 25:147-150(1997).
 RN [11]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=98062175; PubMed=9401003;
 RA Hayward C., Brock D.J.H.;
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
 RT fibrillinopathies.";
 RN Hum. Mutat. 10:415-423(1997).
 RN [12]
 RP VARIANT MFS PRO-1137.
 RX MEDLINE=91304569; PubMed=1852208;
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,
 RA Curristin S.M., Stetten G., Meyers D.A., Francomano C.A.;
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in
 RT the fibrillin gene.";
 RN Nature 352:337-339(1991).
 RN [13]
 RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.
 RX MEDLINE=93250834; PubMed=1301946;
 RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome
 RT patients at cysteine residues in EGF-like domains.";
 RN Hum. Mutat. 1:366-374(1992).
 RN [14]
 RP VARIANT MFS SER-2307.
 RX MEDLINE=92235290; PubMed=1569206;
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
 RT "Marfan phenotype variability in a family segregating a missense
 RT mutation in the epidermal growth factor-like motif of the fibrillin
 RT gene.";
 RN J. Clin. Invest. 89:1674-1680(1992).
 RN [15]
 RP VARIANTS MFS ILE-548 AND ALA-723.
 RX MEDLINE=94010946; PubMed=8406497;
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
 RA Pyeritz R.E., Francomano C.A.;
 RT "Four novel FBN1 mutations: significance for mutant transcript level
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan
 RT syndrome.";
 RN Genomics 17:468-475(1993).
 RN [16]
 RP VARIANT MFS SER-2144.
 RX MEDLINE=93278402; PubMed=8504310;
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 RT disrupt calcium binding of the epidermal growth factor-like module.";
 RN Hum. Mol. Genet. 2:475-477(1993).
 RN [17]
 RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
 RP ALA-1148.
 RX MEDLINE=94108431; PubMed=8281141;
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,
 RA Berg M.A., Miller D.C., Francke U.;
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 RT of five new mutations, including two in 8-cysteine domains.";
 RN Hum. Mol. Genet. 2:1813-1821(1993).
 RN [18]
 RP VARIANTS MFS GLY-217 AND ARG-2627.
 RX MEDLINE=95067970; PubMed=7977366;
 RA Karttunen L., Raghunath M., Lonnqvist L., Peltonen L.;

"A compound-heterozygous Marfan patient: two defective fibrillin
 RT alleles result in a lethal phenotype.";
 RT Am. J. Hum. Genet. 55:1083-1091(1994).
 RN [19]
 RP VARIANT EL LYS-2447.
 RX MEDLINE=94245249; PubMed=8188302;
 RA Lonnqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 RA Peltonen L.;
 RT "A novel mutation of the fibrillin gene causing ectopia lentis.";
 RN Genomics 19:573-576(1994).
 RN [20]
 RP VARIANT MFS CYS-627.
 RX MEDLINE=94272487; PubMed=8004112;
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains
 RT of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
 RT syndrome patients.";
 RN Hum. Mol. Genet. 3:373-375(1994).
 RN [21]
 RP VARIANT MFS CYS-122.
 RX MEDLINE=943114977; PubMed=8040326;
 RA Stahl-Hallengren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 RA Saxne T., Tornqvist K., Peltonen L.;
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth
 RT factor-like motifs of the FBN1 polypeptide is connected to a novel
 RT variant of Marfan syndrome.";
 RN J. Clin. Invest. 94:709-713(1994).
 RN [22]
 RP VARIANT MFS TYR-1223.
 RX MEDLINE=94351682; PubMed=8071963;
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
 RT "A new missense mutation of fibrillin in a patient with Marfan
 RT syndrome.";
 RN J. Med. Genet. 31:338-339(1994).
 RN [23]
 RP VARIANT MFS HIS-1170.
 RX MEDLINE=95174777; PubMed=7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 RT arachnodactyly.";
 RN Mol. Cell. Probes 8:325-327(1994).
 RN [24]
 RP VARIANTS MFS GLY-217; ASN-1023; ARG-1074; TYR-1242; ARG-1513;
 RP GLU-2127; TRP-2151; LYS-2447 AND ARG-2511.
 RX MEDLINE=94184368; PubMed=8136837;
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 RT lentis and neonatal Marfan syndrome.";
 RN Nat. Genet. 6:64-69(1994).
 RN [25]
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 Db 1200 ECSIMNGGCTCTTNSGSEYGCQGFALMPDQSRCT-----DIDE--CEDPNIC 1249
 QY 283 -----DQPGSYSCMCTGYRLAADOHRCEDVDCCILEPSPC-PORCVNTQGFECYCP 335
 Db 1250 DGGQCTNTPGEYRCLCYGFMASEDMKTCVDVNECDLNPNI CLSGTCENTKGSFICHCDM 1309
 QY 336 NYDLVDGE--CPEPVDPC--FRANCEYQCQPLNQI--SVLCVCAEFGA-----PIP 380
 Db 1310 GYSGRKKGKTCTD--INCEIGHNNGKHAIVCTNTAGSFKCSGPGWIGDKICTDLDEGS 1368
 QY 381 HEPHRCQMFNQIACPADCDNPNTQAS--CECEGYILDDGFICTDIDEC-EN-----429
 Db 1369 NGTHMCSQH-----ADC-KNTMGSYRCLCKEYI-TGGDFTCTDLDECSNMLNCGNGQ 1419
 QY 430 -----GGF-----CS-----GVCHNLPGFTEICGPDSPALV 455

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DR EMBL; U69263; AAC51260.2; -
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DR HSSP; P01132; IEGF.
DR Genew; HGNC:6908; MATN2.
DR MIM; 602108; -
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR InterPro; IPR00152; Asx hydroxylase.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; EGF; 10.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00327; VWA_2.
DR PROSITE; PS00010; ASX_HYDROXYL; 9.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS50234; VWF_A; 2.
KW EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
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FT CARBOHYD 221 221
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FT VARSPLIC 861 879
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FT CONFLICT 356 356 /FTid=VSP_001399.
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FT CONFLICT 644 644 V -> E (IN REF. 3).
FT CONFLICT 755 755 R -> G (IN REF. 2).
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Query Match 12.7%; Score 358; DB 1; Length 956;
Best Local Similarity 31.6%; Pred. No. 1.4e-16;
Matches 86; Conservative 41; Mismatches 101; Indels 44; Gaps 15;

QY 227 CSVGNGGCEHACNAIPGAPRCQCPAGALQADGRSCTA-SATQSCNDICEHFCVNPDPQ 285
Db 283 CAMEHDNCEQLCVNVPGSFVQCYSYGVYALAEKRCVAVDYCASNHGCEHCNAD-- 339
QY 286 GSYSCMCEGTGYRLAADQHRCEVDVDCILEPSPQRCQVNTQGGFECHCYNPYDL-VDGEC 344
Db 340 GSYLCQCEHGFALNPKTKTKIDYCASSNHGCOHECVNTDDSYSCHLKGFTLNPKKT 399
QY 345 VEPVDPGF--RANCEYOCQPLNQTSYLCVCAEGFAPIPH-----EPHRCQMF 390
Db 400 CRRINYCALNKPGEHCVCNMEB-SYVCRCHRGYTLDPNGKTCRVVDHCAQDHGCCQLC 458
QY 391 NQTACPADCDPNTQAS--CECPGYILDDGF-ICTDIDEC---ENGFCGVCVCHNLPGTF 444
Db 459 -----LNTEDSFVQCSEGLNEDLKTCSRVDYCLLSDHG--CEYSCVNMDSF 506
QY 445 ECICGPDLSALVRHIGTDCDSKVDG---GDSG 473
Db 507 ACQC-PGHVLRSDGKTC--AKLDSALGDHG 535

RESULT 15
FBL2 MOUSE
ID FBL2 MOUSE STANDARD; PRT; 1221 AA.
AC P37889; Q9WU12;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
GN Fibulin-2 precursor.
OS FBLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=8245130;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding.";
RL J. Cell Biol. 123:1269-1277 (1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization.";
RL Eur. J. Biochem. 263:471-477 (1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=97003230; PubMed=8850569;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo.";
RL Dev. Dyn. 205:348-364 (1996).
RN [4]
RP BINDING TO LAMA2.
RX MEDLINE=99146904; PubMed=10022829;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;

"Binding of the G domains of laminin alpha1 and alpha2 chains and perlecan to heparin, sulfatides, alpha-dystroglycan and several extracellular matrix proteins.";
 RL EMBL J. 18:863-870(1999).

[5]
 RN DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX MEDLINE=21600963; PubMed=11737251;
 RA Gu Y.-C., Tates J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RL fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RT Eur. J. Haematol. 67:176-184(2001).
 CC -!- FUNCTION: Its binding to fibronectin and some other ligands is
 CC calcium dependent.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P37889-1; Sequence=Displayed;
 CC Name=2; Synonym=EGF3-less;
 CC IsoId=P37889-2; Sequence=VSP_001391;
 CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
 CC connective tissues.
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
 CC family contributes to the formation of molecularly distinct
 CC extracellular matrices already during early developmental stages
 CC of a large number of tissues.
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 11 EGF-like domains.

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 DR EMBL; X75285; CAA53040.1; --
 DR EMBL; AF135253; AAD34456.1; --
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 DR EMBL; AF135251; AAD34456.1; JOINED.
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 DR PIR; A49457; A49457.
 DR HSSP; P00736; LAPO.
 DR MGD; MGI:95488; Fbln2.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF00008; EGF; 5.
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 DR SMART; SM00179; EGF_Ca; 9.
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 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS00026; EGF_3; 5.
 DR PROSITE; PS01187; EGF_CA; 10.
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 KW Calcium-binding; Alternative splicing; Repeat.
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 FT DOMAIN 177 434 SUBDOMAIN NB (CYS-FREE).
 FT DOMAIN 435 477 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 478 510 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 511 543 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 594 635 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 669 708 EGF-LIKE 2.
 FT DOMAIN 709 755 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 756 800 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 801 846 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 847 894 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 895 937 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 938 979 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
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 FT DOMAIN 1062 1106 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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 FT CARBOHYD 497 497 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1072 1072 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT S -> L (IN REF. 2).
 FT Q -> QQ (IN REF. 2).
 FT Q -> E (IN REF. 2).
 FT CONFLICT 1102 1102
 FT CONFLICT 1221 AA; 131818 MW; 87DB2A10A8FDC45F CRC64;
 SQ SEQUENCE

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:43:13 ; Search time 37.5 seconds
(without alignments)
4190.082 Million cell updates/sec

Title: US-09-509-994-1_COPY_19_516
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2830	100.0	625	4	Q81V29
2	2654	93.8	468	4	Q9UC32
3	1983.5	70.1	580	6	Q8H248
4	1786	63.1	577	11	O35370
5	1776.5	62.8	491	11	Q8BJB5
6	1396.5	49.3	461	11	P97883
7	574	20.3	652	4	Q81XK1
8	574	20.3	757	4	Q9HCU0
9	566.5	20.0	765	11	Q91ZV1
10	566.5	20.0	765	11	Q91V98
11	433	15.3	1654	5	Q9TVQ2
12	414	14.6	1574	11	O88281
13	385	13.6	1409	5	Q9V889
14	375	13.3	708	13	P87363
15	374	13.2	2906	11	Q9WUH9
16	369	13.0	1231	4	Q81U11

17	369	13.0	1246	4	O75095	O75095 homo sapien
18	367.5	13.0	1184	4	Q86V58	Q86V58 homo sapien
19	366	12.9	3857	11	O88840	O88840 mus musculus
20	365	12.9	2809	4	Q96JP8	Q96JP8 homo sapien
21	365	12.9	2809	4	Q86SJ5	Q86SJ5 homo sapien
22	360	12.7	528	11	Q9CXD8	Q9CXD8 mus musculus
23	360	12.7	2872	11	Q9WUH8	Q9WUH8 rattus norv
24	359	12.7	715	4	Q7Z5X1	Q7Z5X1 homo sapien
25	359	12.7	937	4	Q96FT5	Q96FT5 homo sapien
26	359	12.7	1016	4	Q8NDE6	Q8NDE6 homo sapien
27	358.5	12.7	893	6	Q8MJK0	Q8MJK0 cercopithec
28	358.5	12.7	1174	11	Q99K58	Q99K58 mus musculus
29	357	12.6	590	11	Q8C088	Q8C088 mus musculus
30	356	12.6	1231	4	Q81U10	Q81U10 homo sapien
31	353.5	12.5	746	4	Q96HB9	Q96HB9 homo sapien
32	353.5	12.5	1256	4	Q9NS15	Q9NS15 homo sapien
33	353.5	12.5	1382	4	Q9H7K2	Q9H7K2 homo sapien
34	352.5	12.5	741	4	Q96K89	Q96K89 homo sapien
35	351.5	12.4	1511	4	O75412	O75412 homo sapien
36	351.5	12.4	1587	4	O00508	O00508 homo sapien
37	351	12.4	1666	11	Q8K4G1	Q8K4G1 mus musculus
38	350	12.4	1600	11	Q8K4G0	Q8K4G0 mus musculus
39	346.5	12.2	729	11	Q8BNH3	Q8BNH3 mus musculus
40	346.5	12.2	787	11	Q8K061	Q8K061 mus musculus
41	344.5	12.2	589	13	Q7ZX63	Q7ZX63 xenopus lae
42	343	12.1	5636	4	Q96RW7	Q96RW7 homo sapien
43	341	12.0	576	4	Q9Y3V7	Q9Y3V7 homo sapien
44	338	11.9	1062	11	Q60789	Q60789 mus musculus
45	337.5	11.9	1289	5	Q86AC3	Q86AC3 dictyosteli

ALIGNMENTS

RESULT 1

Q81V29
ID Q81V29 PRELIMINARY; PRT; 625 AA.
AC Q81V29
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; SC035602; AAH35602.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005229; F:sugar binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; ASX hydroxyl_s.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR001491; Thrombomoduln.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00175; EGF; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00041; C TYPE LECTIN_2; 1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01187; EGF_Ca; 2.


```
FT NON TER 1 1
SQ SEQUENCE 625 AA; 65876 MW; 3E5E161183A854B9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2830; DB 4; Length 625;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
DB 69 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 128
QY 61 GGVGRRRLWIGLQPLPPGCGDKPLRGFQWVTGDNNTSYSRWALDLNGLAPLGGPLCV 120
DB 129 GGVGRRRLWIGLQPLPPGCGDKPLRGFQWVTGDNNTSYSRWALDLNGLAPLGGPLCV 188
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHFPATCRPLAVEPGAAAVSITYGTPFA 180
DB 189 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHFPATCRPLAVEPGAAAVSITYGTPFA 248
QY 181 ARGADFOALPVGSSAAVAFLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHACNA 240
DB 249 ARGADFOALPVGSSAAVAFLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHACNA 308
QY 241 IPGAPRCQCPAGALOADGRSCTASATQSCNDLCEHFQVNPDPGYSYCMCETGYRLAA 300
DB 309 IPGAPRCQCPAGALOADGRSCTASATQSCNDLCEHFQVNPDPGYSYCMCETGYRLAA 368
QY 301 DQHRCEVDVDCILPEPSPQPCQVNTQGGFECHCYPNVLDVGECEVPVDPFCFRANCEYQC 360
DB 369 DQHRCEVDVDCILPEPSPQPCQVNTQGGFECHCYPNVLDVGECEVPVDPFCFRANCEYQC 428
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEPGYILDDGFI 420
DB 429 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEPGYILDDGFI 488
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGEPSPS 480
DB 489 CTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVDGSGSGEPSPS 548
QY 481 PTPGSTLTTPPAVGLVHSG 498
DB 549 PTPGSTLTTPPAVGLVHSG 566

RESULT 2
Q9UC32 PRELIMINARY; PRT; 468 AA.
AC Q9UC32;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93293792; PubMed=8390446;
RA Yamamoto S., Mizoguchi T., Tamaki T., Ohkuchi M., Kimura S., Aoki N.;
RT "Urinary thrombomodulin, its isolation and characterization.";
RL J. Biochem. 113:433-440(1993).
DR HSP: P07204; IZAK.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0005509; F:calcium ion binding; IEA.
DR GO: 0005529; F:sugar binding; IEA.
DR GO: 0004888; F:transmembrane receptor activity; IEA.
DR GO: 0007596; P:blood coagulation; IEA.
DR InterPro: IPR00152; Asx_hydroxyl_S.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001304; Lectin_C.
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DR InterPro: IPR001491; Thrombomodulin.
DR Pfam: PF00008; EGF_3.
DR PRINTS: PRO0097; THROMBOMODULN.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00181; EGF; 6.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS00441; C_TYPE_LECTIN_2; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 468 AA; 49444 MW; 4BF8E98EFB86A40 CRC64;

Query Match
Best Local Similarity 93.8%; Score 2654; DB 4; Length 468;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
DB 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
QY 61 GGVGRRRLWIGLQPLPPGCGDKPLRGFQWVTGDNNTSYSRWALDLNGLAPLGGPLCV 120
DB 61 GGVGRRRLWIGLQPLPPGCGDKPLRGFQWVTGDNNTSYSRWALDLNGLAPLGGPLCV 120
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHFPATCRPLAVEPGAAAVSITYGTPFA 180
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHFPATCRPLAVEPGAAAVSITYGTPFA 180
QY 181 ARGADFOALPVGSSAAVAFLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHACNA 240
DB 181 ARGADFOALPVGSSAAVAFLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHACNA 240
QY 241 IPGAPRCQCPAGALOADGRSCTASATQSCNDLCEHFQVNPDPGYSYCMCETGYRLAA 300
DB 241 IPGAPRCQCPAGALOADGRSCTASATQSCNDLCEHFQVNPDPGYSYCMCETGYRLAA 300
QY 301 DQHRCEVDVDCILPEPSPQPCQVNTQGGFECHCYPNVLDVGECEVPVDPFCFRANCEYQC 360
DB 301 DQHRCEVDVDCILPEPSPQPCQVNTQGGFECHCYPNVLDVGECEVPVDPFCFRANCEYQC 360
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEPGYILDDGFI 420
DB 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEPGYILDDGFI 420
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVD 468
DB 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDLSALVRHIGTDCDVGKVD 468

RESULT 3
Q8HZ48 PRELIMINARY; PRT; 580 AA.
AC Q8HZ48;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin precursor.
GN THBD.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Deming C.B., Kim A.Y., Rade J.J.;
RT "Cloning of rabbit thrombomodulin cDNA sequence.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY138902; XAN15931.2; -.
DR FIR: A33308; A33308.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0005509; F:calcium ion binding; IEA.
DR GO: 0005529; F:sugar binding; IEA.
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DR	GO; GO:0004988; P:transmembrane receptor activity; IEA.
DR	GO; GO:0007536; P:blood coagulation; IEA.
DR	InterPro; IPR000152; Asx hydroxyl_S.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR006210; IEGF.
DR	InterPro; IPR001304; Lectin C.
DR	InterPro; IPR001491; Thrombomoduln.
DR	Pfam; PF00008; EGF; 4.
DR	PRINTS; PRO0907; THROMBOMODULN.
DR	SMART; SM00034; CLECT; 1.
DR	SMART; SM00181; EGF; 6.
DR	SMART; SM00179; EGF_CA; 4.
DR	PROSITE; PS00010; ASX HYDROXYL; 2.
DR	PROSITE; PS00041; C TYPE LECTIN_2; 1.
DR	PROSITE; PS01186; EGF 2; 3.
DR	PROSITE; PS01187; EGF_CA; 2.
KW	Signal.
FT	SIGNAL
SQ	SEQUENCE 580 AA; 60115 MW; ABA328FD2E141F42 CRC64;
	Query Match 70.1%; Score 1983.5; DB 6; Length 580;
	Best Local Similarity 71.4%; Pred. No. 4.1e-156;
	Matches 362; Conservative 27; Mismatches 99; Indels 19; Gaps 8
QY	3 AEPPGSGQCVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGDGG 62
DB	23 AEPPDGSGQCVEHDCFALFRGPATFLAAGQTCERLGGHLMTVRSSVAADVLSLLSDDS - 81
QY	63 VGRRLMIGLQLPGCGDKPKELPLRGPFWTGTGNNTSYSPWARLDINGAPLCGPLCVAV 122
DB	82 ---PRLMIGLQPTGCSEHGDLRLRGPFWTGTGNRTSYSPWARQDGGGAPVCGPLCVTV 138
QY	123 SAABATVPSEPIWEQQCEVKADGFLCFEFHPATCRPLAVEPFGAAAA---VSITYGTFP 179
DB	139 SAASAAAPGEPAWEELPGTEVDGFLCFEPFAASCRLPVGAAPATAPHVSSTYTPF 198
QY	180 AARGADQALPVGSSAAVAPLGLQMCTAPGAVGVGHWAREAPCAWDGSVENGGCEHACN 239
DB	199 GARGADFQALPVGSSAAVAPLGLLEITCYAPPFAAEARWGREAPCAWDCSVNGGCEFACN 258
QY	240 AIPCAPPCQCAGAAALQADGSCSTASTAQSCNDICEHCVENPPOPGSVSMCETGYELA 299
DB	259 ASAGAPRLCPDGAAPQADGRSCAAPAPPSCHDICEHFCVNTSDASGYNMCETGYRVA 318
QY	300 ADQHRCEDVDCCILEPSPQPORCVNTQGFECHCVNYDLDVGECVEPDPCFRANCEYQ 359
DB	319 ADGHCEDEVDDCALVPNPCQLCVNTQGFECHCVPGFDLDVGECVELDPFCFCTNCHEYQ 378
QY	360 COPLNOTSYLCVCAEGFAPIPEHRCQMFNCQTACPADCNPNTQASCCEPEGVILDDGF 419
DB	379 CLPLUGQ-NYRICIAEGFAPVDEPHRCQMFNCQTTCPADCDPNYPSTCLCEPEGYILDGGS 437
QY	420 ICTDIDECENGFGCSGVCHNLPGTFPECICGPSDSLVRHIGTDC-----DSKVDGG--DS 472
DB	438 LCADIDECNDN-GYCODECNLPGSYEICIGFPSFLAGOVSTECIPTQVSDGG--DGGDDG 494
QY	473 GSSEPPSPPTPGST-LTPPAVLGVHSQ 498
DB	495 GSSEPPSGAGPSTFPAPPPAAGPVHSQ 521

RESULT 4	
OC035370	PRELIMINARY; PRT; 577 AA.
AC	
DT	01-JAN-1998 (TEMBLrel. 05, Created)
DT	01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT	01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE	Thrombomodulin.
OC	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
Wang J., Yao A., Wang J.Y., Hardin J.W., Hauer-Jensen M.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE OF 1-136 FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
Yao A., Wang J., Hardin J.W., Hauer-Jensen M.;
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF022743; AAB80760.1; -
EMBL; AF022742; AAB80923.1; -
HSP; P07204; 1FGD.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0007586; P:blood coagulation; IEA.
InterPro; IPR000152; Aa: hydroxyl S.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin C.
InterPro; IPR001491; Thrombomodulin.
Pfam; PF00008; EGF; 3.
Pfam; PF00059; Lectin C; 1.
PRINTS; PR00907; THROMBOMODULN.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF CA; 2.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
EGF-like domain.
SEQUENCE 577 AA; 61844 MW; 0BE764CBFF18555F CRC64;

Query Match 63.1%; Score 1786; DB 11; Length 577;
Best Local Similarity 63.7%; Pred. No. 9.7e-140;
Matches 320; Conservative 48; Mismatches 128; Indels 6; Gaps

	Query Match	63.1%;	Score 1786;	DB 11;	Length 577;	
	Best Local Similarity	63.7%;	Pred. No. 9.7e-140;			
	Matches 320;	Conservative 48;	Mismatches 128;	Indels 6;	Gaps 5;	
Qy	1	APAEPOGGGQCVEHDCFALYVGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60			
Dd	19	ALAKLOPKSGCVGNECFALLQDPVTFLDASQAQRLOCHLMTVRSSVAADVISLLVS-D	77			
Qy	61	GGVRRRLWTCLQLPPCGDPPKRLGPLRGFOWTGDNNTSYSRWARLDNGLACPLCPICV	120			
Dd	78	SSMDSRP-WTLQLPQFGCGDPVHLGPLRGFOWTGDNNHTSYSRWARNPDQSFPFLCGCTPCV	136			
Qy	121	AVSAAEAATVPSEPTWEPEQQCEVKADGFLCEPHFPATCRPLAVER-GAAAAVASIITYGTFP	179			
Dd	137	TVSTATAAAGEPAWEKEPCENETKGFCEFYFAAFCEPLRVNTRDPGAHISSTYNPL	196			
Qy	180	AARGADPQALPVSSAAVAPLGILQMCTAPPAGVGHWAREAPCAWDCSVENGCGCEHACN	239			
Dd	197	GVSGADFTQLPIGSSATVAPFGLVLVCRALPGTSEGHWTRVTTGAWNCSVENGGCCEYMKN	256			
Qy	240	AIPCARCCQPAGAALOADGESCTASATQSCNDICEHFVCVNPQPGSYSCMCETGYRLA	299			
Dd	257	RSANGPRVCVPSGGDLQADRGRCAKPVAQLCNELCQHFCVNNSDVPGSYSCMCETGYQLA	316			
Qy	300	ADQHRCEDVDCTILEPSPCFQRCVNTOGGFECHCYPNYDLVDGECVEVPDFCFRANCEVO	359			
Dd	317	ADGHRCEDVDCKQGPNPCPOLCSNTSEGGFECRCIDGYELVDGECVEQLDPCFRSKCBYQ	376			
Qy	360	CQPLNOTSYLVCBAEGFAPIPHEPFRRCMFQNCOTACPADCDDPNTQASCCEPEGYTILDGF	419			
Dd	377	CQPVNSTHYNCICAEGFAPKLDDPDRCEMFCNETSCPADCDDPNSPFQCCPEGFTLDGS	436			
Qy	420	ICTDIDECENGFCSGVCHNLPGTFBICIGPDSALVRHIGTDGSGKV--DGSGSGSGSEP	477			
Dd	437	ICTDIDECSQGECLITNECRNLPGSYECICGPDITALAQIQIKDCDPIPVLEDSGSGSGEH	496			
Qy	478	PPS-PTPGSTLTTPPAVGLVHSG	498			

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Db 497 PSSNPTVSVSTVPSARPMSG 518
Q8BJB5
ID Q8BJB5 PRELIMINARY; PRT; 491 AA.
AC Q8BJB5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK089479; BAC40898.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF_6.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
FT NON TER 491
SQ SEQUENCE 491 AA; 52904 MW; AE2007EEC68AD20D CRC64;

Query Match 62.8%; Score 1776.5; DB 11; Length 491;
Best Local Similarity 67.1%; Pred. No. 5e-139;
Matches 312; Conservative 43; Mismatches 105; Indels 5; Gaps 3;

Qy 1 APAEPQGGSCVHDCFALYPGPATFINASQICDGLRGLHMTVRSSVAADVISLLNGD 60
Db 19 ALAKLQPTGSCVHECFALFQGPATFLDASQAQRQLQHLMTVRSSVAADVISLLSQS 78
Qy 61 G-GVGRRLWIGLQPLPGCGDPKRLGRLPGHWTGDNNTSYSHARLDLNGAPLCPGLC 119
Db 79 SMDLGP--WIGLQPLGCGDDPVHLGLRGLGFWTGDNHTSYSHARPDQAPLCPGLC 135
Qy 120 VAVSAEATVPSEPIWEEQCEVKADGLCFHFHFPATCRPLAVEP-GAAAAVSITYGTP 178
Db 136 VTNSTATEARGEPAWEKPCETETQGLCFEYFTASCRPLVTNTRDPEAAHSSITYNP 195
Qy 179 FAARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGGBHAC 238
Db 196 FGVSADFTQLPVGSSAAVEPLGLVLCRAPPGTSEGHWAREATGANNCVENGGBEYLC 255
Qy 239 NAIFGARPCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSCMETGYRL 298
Db 256 NRSTNEPRCLCPDMDLQADGRSCARPVVQSCNLCHEHFCVNSAEVPGSYSCMETGYQL 315
Qy 299 AADQHRCEVDVDCILEPSPQPCORCVNTGGFECCHYCNVLDVQCEVPEPDPCCFRANCEY 358
Db 316 AADQHRCEVDVDCQKQGNPCFLQVNTKGGFEFCFYDGYELVDGECVELLDPCFGSNCF 375

Qy 359 QCOPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCECPGYYILDG 418
Db 376 QCOQVFTDYRCICAPGFAPKPDPEPHKCFMFCNETSPADCDNSPTVCPCPGFILDG 435
Qy 419 FICTIDECENGFCGVCVCHNLPGTFECICGDPDSALVRHIGTDCD 463
Db 436 SVCTIDECESQCECTSECRNFSGSYECICGPDPTALAGQISKDCD 480

RESULT 6
P97883
ID P97883 PRELIMINARY; PRT; 461 AA.
AC P97883;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Brain capillary;
RC Wang L., Tran N.D., Schreiber S.S., Zickovic B.V.;
RA "Nucleotide sequence of rat thrombomodulin.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90121; AAB49723.1;
DR HSPB; P07204; 1FGD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF_3.
DR PRINTS; PR00907; THROMBOMODULIN.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
FT NON TER 1
SQ SEQUENCE 461 AA; 49499 MW; 45971BCE84688B67 CRC64;

Query Match 49.3%; Score 1396.5; DB 11; Length 461;
Best Local Similarity 62.4%; Pred. No. 1.5e-107;
Matches 244; Conservative 37; Mismatches 105; Indels 5; Gaps 4;

Qy 113 PLGCLPCLVAVSAEATVPSEPIWEEQCEVKADGLCFHFHFPATC-RPLAVEP-GAAAA 170
Db 12 PLGCLPCLVTVSTATEARGEPAWEKPCENETKGLCFEYFAAFCSRPLRVNTRDPEGAH 71
Qy 171 VSTYTGTPFAARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSV 230
Db 72 ISSTYTVPLGVSGADFTPLIGSSATVAPFGLVLCRALPGTSEGHWTREVTGAWNCVSE 131
Qy 231 NGGCEHACNAIPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSC 290
Db 132 NGGCEYMCNRSANGPRCVCPSGGDLQADGRSCKAPVQLCNELCQHFVNNSDVPGSYSC 191
Qy 291 MCTGYRLAADQHRCEVDVDCILEPSPQPCORCVNTGGFECCHYCNVLDVQCEVPEPDP 350
Db 192 MCTGYRLAADQHRCEVDVDCQKQGNPCFLQVNTGGFECCHYCNVLDVQCEVPEPDP 251
Qy 351 CFRANCEYCOPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCECP 410
Db 252 CFRANCEYCOPLNQTSYLCVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCECP 311
Qy 411 EGYLDDGFTCTIDECENGFCGVCVCHNLPGTFECICGDPDSALVRHIGTDCDSGKV--D 468

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Db 312 EGFILDESGICTDIDECQGECLTNECRNLPGSYECIGPDTALAGQISKDCDDIPVLED 371
QY 469 GDSGSGEPPPS-PTPGSTLTTPRAVLVHSG 498
Db 372 SEDGSGEHPSSNFTVVSSTVPPSPARPMHSG 402

RESULT 7
Q8IXK1
ID Q8IXK1 PRELIMINARY; PRT; 652 AA.
AC Q8IXK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Clq receptor protein precursor.
GN CD93.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Steinberger P., Stoeckl J., Wille S., Szekeres A., Prager E.,
RA Staffier G., Kuenig S., Kohl P., Majdic O., Knapp W., Stockinger H.;
RT "Identification of CD93 as the Clq receptor protein (ClqR) by
RT retroviral expression cloning.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295142; CAC82720.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR00152; ASX_HYDROXYL_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF01108; Tissue_fac; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 5.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
KW Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 652 C1Q RECEPTOR PROTEIN.
SQ SEQUENCE 652 AA; 68521 MW; 97549BA62CAF225E CRC64;

Query Match
Best Local Similarity 31.4%; Pred. No. 3,6e-39;
Matches 174; Conservative 52; Mismatches 202; Indels 126; Gaps 31;

QY 6 QPGSGQ-----CVHEPCFALYPGATFNLNASQICDGLRGHLMTVRSVAAD-----VI 53
Db 17 QPGAGTGADTEAVVCVGTACTYATSHSGKLSAAEQNHQNGNLATVKSKEAQHVQRVL 76
QY 54 SLILNGDGGVGR--RLWIGLQLPPG--CGDPKRLGLRGLFQWVTGDNNNTYSRWARLDLN 110
Db 77 AQLLRRAALFARMSKFWIGLQREKGLDPSL--PLKGFSGWGGEDTPTYSNNHKELRN 134
QY 111 GAPLCGFLCVA--VSAEAATVPS--PIWEQOC-----EVKADGFLCEFFHFPATCRPLA 161
Db 135 SC--ISKRCVSLLDLSQPLLPSRLPKWSEGPCSGSPGSGNIEGFVCKFSFKGMCEPLA 192
QY 162 V-EFGAAAASVITYGTPFPAARGADFOALPVGSSAAVAPLGLQMC--TAPFGAVQGHW-- 217
Db 193 LGGFG-----QVITYTTPFTQTSLSLEAVFPASAANVA-----CGEGDKDETQSHYFL 239

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QY 218 -AREAPGAWD-----CSVENGCGCEHAC-NAIPGAPRCOCPIGALQADGRS 261
Db 240 CKEKAPDVFDMGSSGSLCVSPKYGCMFNNGGCHQDCFEFGDGSFLCGCRFGRLLDLVT 299
QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSYCMCEGYRLAADOHRCEDVDDCILLESPPCP 319
Db 300 C-ASRNPPCSSPCRGATCALGP-HGKNYTCRCPQGYQLDSSQLDQDVDEEC--QDSPCA 355
QY 320 QRCVNTQGGFECHYCNPNYDLVDGECVEPDPFCFRANCEYQCQPLNQTSYLCVCAEGFAP 379
Db 356 QECVNTPGGPRCBWVGY-----EPGGP-----GEGACQDVDE-----CALGRSP- 395
QY 380 PHEPHRCQMECNQTACPADCDPNTQAS--CECPEGYL--DDGFICTDIDEC--ENGGFC 433
Db 396 -----CAQGC-TNTDGSFHCSCEGYVLAGEDGTQCQDVDECVGPGGPLC 439
QY 434 SGVCHNLPGTFECICQGPSALVRHIGTDCDSGKV-----DGGDSGSGE-----P 477
Db 440 DSLCFNTQSSFHCGCLPGWVLAEN-GVSCMTMGVSLGPPSGPPDEEDKGEKGVTPRAA 498
QY 478 PPSPTPGSTLTTPPA 491
Db 499 TASPTRGPGEGTPKA 512

RESULT 8
Q9HCUC0
ID Q9HCUC0 PRELIMINARY; PRT; 757 AA.
AC Q9HCUC0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor endothelial marker 1 precursor (Endosialin protein).
GN TM1 OR ENDOSIALIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery B., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium.";
RN Science 289:1197-1202(2000).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=21269274; PubMed=11084048;
RA Christian S., Ahorn H., Koehler A., Eisenhaber F., Rodi H.P.,
RA Garin-Chesa P., Park J.E., Rettig W.J., Lenter M.C.;
RT "Molecular cloning and characterization of Endosialin, a C-type
RT lectin-like cell surface receptor of tumor Endothelium.";
J. Biol. Chem. 276:7408-7414(2001).
DR EMBL; AF279142; AAG00867.1; -.
DR EMBL; AJ295846; CAC34381.1; -.
DR HSP; P07204; IZAQ.
DR Genew; HGNC:18219; CD164L1.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR InterPro; IPR00152; ASX_HYDROXYL_S.
DR InterPro; IPR001891; EGF_CA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain; Signal.

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Qy	180	AARGADPQALFVGSNAV---APLGLQLMCTAPPAGVAQHWAREAP--GAWDCSVENGGC	234
Dd	184	NVSSEFEWLPTFGSAAVQCQAGRGAASLLCVKQPSSGVG-WSQTGPLCPGTGCSPDNGGC	242
Qy	235	EHAC-NAIPGAPRCOCPACAALQAQDGSRSTASATQS-CNDLCBHFCVPNPDQPGSYSQMC	292
Dd	243	EHECVEVDGANVCSCSEGFRILAADSHSCDPCAQACPQQCB-----PGGFQGISCHC	296
Qy	293	ETGYRLAADI-HRCEVDVDDCILPEPSPCQRVNTQGGECHCYPNYDL-VDGECVEP	347
Dd	297	RLGFRPAEDPHRCVDTDECQI-AGVCQMCMVNYYVGGEFCYCSGEGHELEADGISCS	352
 RESULT 11 Q9TVQ2 PRELIMINARY; PRT; 1664 AA.			
ID	Q9TVQ2;		
AC	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Y64GI0A.7		
DE	Y64GI0A.7 GN		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
ON	NCBI_TaxID=6239;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RA	Mortimore B.J.;		
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=99069613; PubMed=9851916;		
RA	none;		
RT	"Genome sequence of the nematode C.elegans: A platform for		
RT	investigating biology";		
RT	Science 282:2012-2018 (1998).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Ainscough R.;		
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AL117206; CAB60454.1; -		
DR	EMBL; AL110498; CAB60454.1; JOINED.		
DR	EMBL; AL110498; CAB57911.1; -		
DR	EMBL; AL117206; CAB57911.1; JOINED.		
DR	HSSP; P00736; IAPQ.		
DR	WormPeP; Y64GI0A.7; CE24549.		
DR	GO; GO:0005509; Fcalcium ion binding; IEA.		
DR	GO; GO:0005198; Fstructural molecule activity; IEA.		
DR	InterPro; IPRO00152; Asx hydroxyl_S.		
DR	InterPro; IPRO01881; EGF_Ca.		
DR	InterPro; IPRO06209; EGF_like.		
DR	InterPro; IPRO02049; Laminin_EGF.		
DR	Pfam; PF00008; EGF; 22.		
DR	PRINTS; PR00011; EGFLAMININ.		
DR	SMART; SM00179; EGF CA; 4.		
DR	PROSITE; PS00010; ASX HYDROXYL; 4.		
DR	PROSITE; PS00022; EGF_1; 22.		
DR	PROSITE; PS01186; EGF^2; 24.		
DR	PROSITE; PS01187; EGF_CA; 3.		
KW	EGF-like domain.		
SQ	SEQUENCE 1664 AA; 179279 MW; A69F093B4C705832 CRC64;		
 Query Match 15.3%; Score 433; DB 5; Length 1664; Best Local Similarity 29.7%; Pred.No.5e-27; Matches 126; Conservative 41; Mismatches 177; Indels 80; Gaps 19;			
Qy	101	YSRWALDLNGAPLCPGLCVAVSAAE-----ATVPSEPIWEQQCE--VKADGFLCEF	151
Dd	56	YLAFANFSRRGCKCLLRVOANCSDLLCHNGGTCTVPSSEHNDEQVCECPVFTGAKQY	115
Qy	152	HFPATCRPLAVEPGAAAAVAISITVTGTFFAARGADFALPVGSSAAVAPLQLMCTAPP	211

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Celisner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Buesam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA Mcintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

RN SEQUENCE FROM N.A.
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]

RN SEQUENCE FROM N.A.
 RP FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AEO03558; F050538.2;
 DR HSSP: P00736; IAPQ.
 DR FlyBase: F8m0035798; CG7526.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO: GO:0007596; P:blood coagulation; IEA.
 DR InterPro: IPR000152; Asx hydroxylase.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR003410; Hyalin.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR InterPro: IPR001491; Thrombomodulin.
 DR Pfam: PF00008; EGF; 11.
 DR Pfam: PF00084; sushi; 2.
 DR PRINTS: PR00907; THROMBOMODULN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00181; EGF; 13.
 DR SMART: SM00179; EGF_Ca; 14.
 DR PROSITE: PS00010; ASX_HYDROXYL; 8.
 DR PROSITE: PS01186; EGF_2; 9.
 DR PROSITE: PS01187; EGF_Ca; 10.
 KW EGF-like domain.
 SQ SEQUENCE 1409 AA; 154131 MW; F9A0DE1478AF354C CRC64;

Query Match 13.6%; Score 385; DB 5; Length 1409;
 Best Local Similarity 32.1%; Pred. No. 4e-23;
 Matches 99; Conservative 33; Mismatches 110; Indels 66; Gaps 18;

QY 206 CTAPFGAVQG-----HWAREAPGAW-----DCSVNGGCEHACNAIPG 243

Db 563 CLCPGGYALGLDNHIVTSLNGSFITDSTSTSPSAHTCLDIDECSLANGNSHFQCNBPG 622
 QY 244 APRCOCAGALQADGRSCTASATQSC---NDLCEHFVCPNPDPGSGYSCMCETGVRLAA 300
 Db 623 GFQACACPLGYALSEDMRTC--QDIDECUDSGQCSQLCL---NQPGGFACACETGFELTP 677
 QY 301 DOHRCEDVDDCILEPSPCPQRCVNTQGGFCHCYPNYDLVDGE--CVFVDPFC---FRAN 355
 Db 678 DDFGADIDEGSDYNGXGSDICINLLGTHACACRGYELAKDKLSCLD-VDECAGLLSG 736
 QY 356 CEYQCQPLNQT-SYLCVCAEGFAPIPHPHRCQMFNCOTACPA--DCDPNTQASC----- 407
 Db 737 CSHEC--INKAGTFECGCPGAG--ILNDG-----SCSPALVGCPPGTORSADGCAP 785
 QY 408 -PCPGYILDDGFICTDIDEC--ENGGRCSGVCHNLPGTFECICGPF-----DSALVRHI 458
 Db 786 IECNFGYTLGSDKCDVIDEOKQNGG-CSHRCSNTEGSKFCSPGPGYELDSQDKTCQDI 844
 QY 459 GTDCDSGK 466
 Db 845 -DECQDQK 851

RESULT 14

P87363
 ID P87363 PRELIMINARY; PRT; 708 AA.
 AC P87363;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibrillin-1 (Fragment).
 GN FBNI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20152896; PubMed=10691037;
 RA Zhou G., Price C.E., Rosenquist T.H., Gadsen P.F., Godfrey M.;
 RT "Partial cloning and sequencing of chick fibrillin-1 cDNA.";
 RL In Vitro Cell. Dev. Biol. Anim. 36:19-25(2000).
 DR EMBL: U88872; AAB48531.1; -.
 DR HSSP: P07204; 2ADX.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR000152; Asx hydroxylase.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR002212; Fibril-assoc.
 DR Pfam: PF00008; EGF; 13.
 DR Pfam: PF00683; TB; 2.
 DR SMART: SM00179; EGF_Ca; 14.
 DR PROSITE: PS00010; ASX_HYDROXYL; 13.
 DR PROSITE: PS01186; EGF_2; 10.
 DR PROSITE: PS01187; EGF_Ca; 13.
 KW EGF-like domain.
 FT NON TER 708
 SQ SEQUENCE 708 AA; 76164 MW; C247271C1DF73361 CRC64;

Query Match 13.3%; Score 375; DB 13; Length 708;
 Best Local Similarity 31.8%; Pred. No. 1.2e-22;
 Matches 112; Conservative 26; Mismatches 108; Indels 106; Gaps 20;

QY 226 DCSVNGGCEHACNAIPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFVCPNP--- 282
 Db 223 ECSIMNGGCENFCTSGSEYECSCQGFALMPDHTCT-----DIDB--CEDNPIC 272
 QY 283 -----DQPGSYSCMCETGVRLAADQHRCEVDVDCILEPSPC-PQRCVNTQGGFCHCY 335
 Db 273 DGGQCTNIPGEYRCLCVDFGNASEDMKTCVDVNECDLHFNICLSGTCENTKGSFICHCDM 332


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QY 336 NYDLVGE--CVPSPVDP--FRANCEYQCQPLN-QTSYLCVCAEGFA-----PIP 380
Db 333 GYSGKKGTCTD-INECEIGAHCNDRHAVCTNIPGSFKSCSSGMIKGTDLDECS 391
QY 381 HEPHRCOMFCNQACPADCPNTQAS--CECPGYILDDGFICTDIDE-----CENG- 430
Db 392 NGTHKCSPH-----ADC-KNTMGSYRCLCKEGY-TGDGFTCTDLDCESENINLCENGQ 442
QY 431 -----GF-----CS-----GVCHNLPGTFFECICGPDPSALV 455
Db 443 CLNAPGGYRCEDMGFLPSLDGKACEIDECSLPNICVYGTCNLPGLFRCECEBGVELD 502
QY 456 RHIG-----TPCDGSK-VGDGSGSGEPPPTGSGTLTPPAVGLV 495
Db 503 RSGNCTDVNECAPTTCTISGTCVNTAGSYTCECPDP-----FELNPRVGCV 550
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RESULT 15
Q9WUH9 PRELIMINARY; PRT; 2906 AA.
AC Q9WUH9;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fibrillin-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99350231; PubMed=10419698;
RA Yang O., Ota K., Tian Y., Kumar A., Wada J., Kashiwara N., Wallner E.,
RA Kanwar Y.S.;
RT "Cloning of rat fibrillin-2 cDNA and its role in branching
RT morphogenesis of embryonic lung.";
RL Dev. Biol. 212:229-242 (1999).
DR EMBL; AF135060; AAD34439.1; -.
DR HSSP; P35555; 1EMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF_44.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS01187; EGF_CA; 43.
KW EGF-like domain.
SQ SEQUENCE 2906 AA; 313371 MW; 9EB64E727044EF58 CRC64;
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Query Match 13.2%; Score 374; DB 11; Length 2906;
Best Local Similarity 32.9%; Pred. No. 7.3e-22;
Matches 102; Conservative 24; Mismatches 92; Indels 92; Gaps 18;

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QY 226 DCSVENGCEHACNAIPGAPPCQAGALQADGRSCTASATQSCNDLCEHFCVNPED-- 283
Db 1237 ECTMNGGCDTQCTNSGSEYSCSGSEGYALMPDGRSCA-----DIDE--CENNPDIC 1286
QY 284 -----QPSYSQWCETGYRLADQHRCEVDVDCILEPSCP-QRCVNTQGGFECHCYP 335
Db 1287 DGGQCTNIPGBYRCLCYDGFNASMDMTCTIDVNECDLNPICMPGECENTKGSFICHQQL 1346
QY 336 NYDLVGE--CVPSPVDP--FRANCEYQCQPLN-QTSYLCVCAEGFA-----PIP 380
Db 1347 GYSVKKGATGCTD-VDECEIGAHCNDRHAVCTNIPGSFKSCSSGMIKGTDLDECA 1405
```

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QY 381 HEPHRCOMFCNQACPADCPNTQAS--CECPGYILDDGFICTDIDE-----CENG- 430
Db 1406 NGTHQCSI-----NAQC-VNTPGSYRCACSEGF-TGDGFTCSDDYDECAENINLCENGQ 1456
QY 431 -----GF-----CS-----GVCHNLPGTFFECICGPDPSALV 455
Db 1457 CLNVPGAYRCECEMGFTPASDSRSCQDIDECSPONICVEGTCNNLPQMFHCICDDGYGLD 1516
QY 456 RHIG--TDGD 463
Db 1517 RTGGHCTDID 1526
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Search completed: June 9, 2004, 08:49:59
Job time : 40.5 secs

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OM protein - protein search, using sw model
Run on: June 9, 2004, 08:39:53 ; Search time 53.5 Seconds
(without alignments)
2630.068 Million cell updates/sec

Title: US-09-509-994-2_COPY_19_516
Perfect score: 2830
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq_29Jan04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2830	100.0	516	AAY09348	Aay09348 Human thr
2	2830	100.0	516	AAY83935	Aay83935 Human thr
3	2830	100.0	516	ABU08703	Abu08703 Thrombomo
4	2830	100.0	516	ADA37275	Ada37275 Human sol
5	2830	100.0	575	ABG72575	Abg72575 Human thr
6	2830	100.0	575	ABM78950	Abm78950 Breast ca
7	2830	100.0	575	ADE54760	Ades54760 Human Pro
8	2830	100.0	575	ADD48168	Add48168 Human Pro
9	2830	100.0	631	ABG72572	Abg72572 Human thr
10	2826	99.9	498	AAR84185	Aar84185 Human der
11	2826	99.9	498	AAW01600	Aaw01600 Thrombomo
12	2826	99.9	498	AAW167402	Aaw167402 Novel sug
13	2826	99.9	516	AAR22016	Aar22016 Truncated
14	2826	99.9	516	AAY09347	Aay09347 Human thr
15	2826	99.9	516	AAAY83934	Aay83934 Human thr
16	2826	99.9	516	AAAY69529	Aay69529 Human thr
17	2826	99.9	516	ABU08701	Abu08701 Thrombomo
18	2826	99.9	516	ADA37271	Ada37271 Human thr
19	2826	99.9	575	AAR11534	Aar11534 Human thr
20	2826	99.9	575	AAR41806	Aar41806 Thrombomo
21	2826	99.9	575	AAAE17521	Aae17521 Human thr
22	2826	99.9	575	AAAE17521	Aae17521 Human ful
23	2826	99.9	575	AAAE23026	Aae23026 Human thr
24	2824	99.8	497	AAR94607	Aar94607 Human rec
25	2824	99.8	515	AAR10617	Aar10617 Soluble t

ALIGNMENTS

RESULT 1

AAAY09348	AAAY09348 standard; protein; 516 AA.
XX	XX
AC	AAAY09348;
XX	XX
DT	08-JUL-1999 (first entry)
XX	XX
DE	Human thrombomodulin SEQ ID NO:2.
XX	XX
KW	Human; thrombomodulin; aqueous parenteral solution; storage; distribution; acute coronary syndrome; thrombosis; embolism; diabetes.
KW	Human; thrombomodulin; aqueous parenteral solution; storage; distribution; acute coronary syndrome; thrombosis; embolism; diabetes.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO9918994-A1.
XX	XX
PD	22-APR-1999.
XX	XX
PF	13-OCT-1998; 98WO-JP004609.
XX	XX
PR	15-OCT-1997; 97JP-00281659.
PR	11-NOV-1997; 97JP-00308523.
XX	XX
PA	(ASAH) ASAH KASEI KOGYO KK.
PI	Yui M, Yokozawa A, Murata T, Tsuruta K, Shimizu H;
XX	XX
DR	WPI; 1999-277444/23.
XX	XX
PT	Stable aqueous parenteral thrombomodulin solution - comprising buffer and surfactant, useful for treating acute coronary syndrome, thrombosis, embolism, and diabetes.
XX	XX
PS	Claim 7; Page 90-92; 97pp; Japanese.
XX	XX
CC	The present invention describes a method for maintaining the quality of an aqueous parenteral solution of thrombomodulin comprising buffer and surfactant aseptically filled in a case or syringe. Maintaining the quality of an aqueous, parenteral thrombomodulin solution is characterised in that the solution: (a) comprises soluble thrombomodulin, a buffer to maintain the pH at 5-7 and a surfactant; (b) is aseptically filled into: (i) a case or (ii) a syringe without any empty space; and (c) is kept in liquid form in storage and distribution and not frozen or freeze dried. Thrombomodulin is used to treat acute coronary syndrome (such as myocardial infarction, unstable angina and coronary artery blockage), thrombosis (e.g. cerebral, vascular and peripheral blood

CC vessel thrombosis), embolism, peripheral blood vessel disorders (e.g.
CC Raynaud's disease), arteriosclerosis, vasculitis (e.g. due to systemic
CC lupus erythematosus or Barret's syndrome), multiple organ failure,
CC disseminated intravascular coagulation, transient ischaemia, diabetes,
CC liver veno-occlusive diseases and deep vein thrombosis. The composition
CC is stable for a long period of time and can be stored and distributed in
CC ready to use form avoiding the problems of dissolution and accuracy when
CC preparing on demand. The present sequence represents human thrombomodulin
XX
XX Sequence 516 AA;
SO

Query Match	100.0%;	Score 2830;	DB 2;	Length 516;	
Best Local Similarity	100.0%;	Pred. No. 7,5e-150;			
Matches 498;	Conservative	0;	Mismatches	0;	Indels
				0;	Gaps
					0;

QY	1	APAEPPGGSQCV	EHDCF	FALYPG	PAIFL	NASQICDGLR	GHLMTV	RSVAAD	VISLL	NGD	60
DB	19	APAEPPGGSQCV	EHDCF	FALYPG	PAIFL	NASQICDGLR	GHLMTV	RSVAAD	VISLL	NGD	78
QY	61	GGVGRRLTWGLQ	LPPCG	DPKRLG	PLRG	QWWTG	DNNTSY	SRWRLD	NGALC	GPLCV	120
DB	79	GGVGRRLTWGLQ	LPPCG	DPKRLG	PLRG	QWWTG	DNNTSY	SRWRLD	NGALC	GPLCV	138
QY	121	AVSAAEATV	PSPTW	ESQCEV	KADGFL	CRFH	FPATCR	PLAVEP	GAAGAAA	VSYTYG	180
DB	139	AVSAAEATV	PSPTW	ESQCEV	KADGFL	CRFH	FPATCR	PLAVEP	GAAGAAA	VSYTYG	198
QY	181	ARGADFOAL	PVGSSAA	VAPLGL	QLMCTAP	PGAVQ	GHWARE	APGAWD	CSVENG	GCHEA	240
DB	199	ARGADFOAL	PVGSSAA	VAPLGL	QLMCTAP	PGAVQ	GHWARE	APGAWD	CSVENG	GCHEA	258
QY	241	IPGAPRCQ	PAGAA	LQADGR	SCTASATQ	SCNDL	CEHFCV	PNPDQ	BGSYS	CMCETGY	300
DB	259	IPGAPRCQ	PAGAA	LQADGR	SCTASATQ	SCNDL	CEHFCV	PNPDQ	BGSYS	CMCETGY	318
QY	301	DQHRCEDV	DDCIL	BSPCPQ	RCVNTQ	GGFE	CHCYPNY	DLV	DGCEV	PDVPC	360
DB	319	DQHRCEDV	DDCIL	BSPCPQ	RCVNTQ	GGFE	CHCYPNY	DLV	DGCEV	PDVPC	378
QY	361	QPLNOTSV	LCVCAE	GFAP	IPHEP	HR	COMFCN	TACPAD	CDPNTQ	ASCE	420
DB	379	QPLNOTSV	LCVCAE	GFAP	IPHEP	HR	COMFCN	TACPAD	CDPNTQ	ASCE	438
QY	421	CTDIDECENG	FCSGV	CHNLPT	GFEC	ICG	PDSSAL	ARHICTD	CSKVD	G	480
DB	439	CTDIDECENG	FCSGV	CHNLPT	GFEC	ICG	PDSSAL	ARHICTD	CSKVD	G	498
QY	481	PTPGSTL	TPP	AVGL	VHSG	498					
DB	499	PTPGSTL	TPP	AVGL	VHSG	516					

RESULT 2	
AAy83935	
ID	AAy83935 standard; protein; 516 AA.
XX	
AC	AAy83935;
XX	
DT	28-JUL-2000 (first entry)
XX	
DE	Human thrombomodulin TMD protein #2.
XX	
KW	Human; thrombomodulin; vasculitis; protein C; thrombin.
XX	
OS	Homo sapiens.
XX	
PN	JP2000053582-A.
XX	
PD	22-FEB-2000.
XX	
PF	06-AUG-1998; 98JP-00222688.
XX	
PR	06-AUG-1998; 98JP-00222688.
XX	

XX (ASAH) ASahi KASEI KOGYO KK.
XX WPI; 2000-353249/31.
XX N-PSDB; AAA10028.
XX Treating agent for vasculitis contains peptide which promotes activation
XX of protein C by thrombin.
XX Claim 4; Page 13-14; 18pp; Japanese.
XX This sequence represents a human thrombomodulin protein. The invention
XX relates to a treating agent for vasculitis containing a peptide which
XX promotes activation of protein C by thrombin
XX Sequence 516 AA;
XX

Query Match	100.0%;	Score 2830;	DB 3;	Length 516;
Best Local Similarity	100.0%;	Pred. No. 7.5e-150;	Indels 0;	Gaps 0;
Matches 498;	Conservative 0;	Mismatches 0;		
Qy	1	APAEPQGSQCVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60	
Db	19	APAEPQGSQCVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	78	
Qy	61	GGVGRRLTWIGLQPLPGCGDPRKELGRLRQFQWVTGDNNTSYSRWARLDLNGAPLCPLCV	120	
Db	79	GGVGRRLTWIGLQPLPGCGDPRKELGRLRQFQWVTGDNNTSYSRWARLDLNGAPLCPLCV	138	
Qy	121	AVSAAEATVPSEPIWEBOQCEVKADGFLCEHFHPATCRPLAVPGAAAAVSYTGTFFA	180	
Db	139	AVSAAEATVPSEPIWEBOQCEVKADGFLCEHFHPATCRPLAVPGAAAAVSYTGTFFA	198	
Qy	181	ARGADFQALPVGSSAAVAPILGLQMLCTAPCAVQGHWAREAPGAWDCSVENGGEHA	240	
Db	199	ARGADFQALPVGSSAAVAPILGLQMLCTAPCAVQGHWAREAPGAWDCSVENGGEHA	258	
Qy	241	IPGAPRCQCPAGAAQLQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSCMCETGYLAA	300	
Db	259	IPGAPRCQCPAGAAQLQADGRSCTASATQSCNDLCEHFCVNPDPQSGYSCMCETGYLAA	318	
Qy	301	DQHRCEDVDICILBSPQPCQVNTQGGFECHCPYNDLVGECVEVPDPCFRANCEYQC	360	
Db	319	DQHRCEDVDICILBSPQPCQVNTQGGFECHCPYNDLVGECVEVPDPCFRANCEYQC	378	
Qy	361	QPLNQTSYLCVCAEGFAPLIPHEPHRCQMFNCQTACFADCDPNTQASCPCPGYILDDGFI	420	
Db	379	QPLNQTSYLCVCAEGFAPLIPHEPHRCQMFNCQTACFADCDPNTQASCPCPGYILDDGFI	438	
Qy	421	CTDIDECENGGFCSGVCHNLPGTFFCICGPDSSALARHIGTDCDSKVDGSGSGSGEPPPS	480	
Db	439	CTDIDECENGGFCSGVCHNLPGTFFCICGPDSSALARHIGTDCDSKVDGSGSGSGEPPPS	498	
Qy	481	PTFGSTLTTPPAGVLVHSG	498	
Db	499	PTFGSTLTTPPAGVLVHSG	516	

RESULT 3	
ABU08703	
ID	ABU08703 standard; protein; 516 AA.
XX	
XX	
AC	ABU08703;
XX	
XX	
DT	17-JUN-2003 (first entry)
XX	
XX	
DE	Thrombomodulin-containing composition associated protein #3.
XX	
XX	Thrombomodulin; antiplatelet; anticoagulant; thrombolytic;
KW	blood coagulation-fibrinolysis system; vascular obstruction;
KW	myocardial infarction; acute coronary syndrome; brain infarction; sepsis;
KW	cardiac; cerebroprotective; antibacterial; immunosuppressive;
KW	anticoagulant; thrombolytic.

XX OS Unidentified.
 XX PN WO2003013606-A1.
 XX PD 20-FEB-2003.
 XX PF 07-AUG-2002; 2002WO-JP008058.
 XX PR 08-AUG-2001; 2001JP-00241371.
 XX PA (ASAH) ASAH KASEI KOGYO KK.
 XX PI Suzuki H, Mohri M;
 XX DR WPI; 2003-248241/24.
 XX DR N-PSDB; ABX94089.
 XX PT Thrombomodulin-containing medicinal compositions useful for treating or
 PT preventing e.g. myocardial infarction, brain infarction, acute coronary
 PT syndrome and sepsis.
 XX PS Claim 18; Page 34-37; 48pp; Japanese.
 XX CC The invention describes drug compositions containing thrombomodulin, and
 CC an antiplatelet, an anticoagulant or/ and a thrombolytic other than
 CC thrombomodulin. The drug compositions are for preventing or treating
 CC diseases or syndromes due to abnormality in the blood coagulation-
 CC fibrinolysis system or/ and vascular obstruction, including myocardial
 CC infarction, acute coronary syndrome, brain infarction and sepsis,
 CC particularly as combination drug compositions. The compositions have high
 CC therapeutic efficacy. This is the amino acid sequence of a thrombomodulin
 CC -containing composition associated protein
 XX SQ Sequence 516 AA;
 XX
 Query Match 100.0%; Score 2830; DB 6; Length 516;
 Best Local Similarity 100.0%; Pred. No. 7.5e-150;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISLLNGD 60
 DB 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISLLNGD 78
 QY 61 GGVGRRRLWTGLQPPCGGPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 DB 79 GGVGRRRLWTGLQPPCGGPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPTWEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAVSIYGTFFA 180
 DB 139 AVSAAEATVPSEPTWEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAVSIYGTFFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 240
 DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 258
 QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVPNPDPQPGSYSCMCETGYRLAA 300
 DB 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVPNPDPQPGSYSCMCETGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPCPCQRCVNTQGGFCHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
 DB 319 DQHRCEVDVDCILEPSPCPCQRCVNTQGGFCHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 378
 QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQTACPADCDPNTQASCECEGYIILDDGFI 420
 DB 379 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQTACPADCDPNTQASCECEGYIILDDGFI 438
 QY 421 CTTDIDCEGNGGFCGVCNHLPGTFECICGPDLSALARIHIGTDCDSKGVGDGSGSGEPFPPS 480
 DB 439 CTTDIDCEGNGGFCGVCNHLPGTFECICGPDLSALARIHIGTDCDSKGVGDGSGSGEPFPPS 498
 QY 481 PTFGSTLTTPPAVGLVHSG 498

DB 499 PTFGSTLTTPPAVGLVHSG 516
 RESULT 4
 ADA37275
 ID ADA37275 standard; protein; 516 AA.
 XX AC ADA37275;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human soluble thrombomodulin protein SEQ ID NO:5.
 XX KW high-concentration preparation; soluble thrombomodulin; human;
 XX KW thrombomodulin.
 XX OS Homo sapiens.
 XX OS WO2003061687-A1.
 XX PN 31-JUL-2003.
 XX PD 17-JAN-2003; 2003WO-JP000339.
 XX PF 18-JAN-2002; 2002JP-00009951.
 XX PR (ASAH) ASAH KASEI KK.
 XX PI Nishio F;
 XX DR WPI; 2003-712487/67.
 XX DR N-PSDB; ADA37276.
 XX PT High concentration stable low-foaming soluble thrombomodulin preparation
 PT for pharmaceutical use.
 XX PS Claim 18; Page 102-104; 113pp; Japanese.
 XX CC The present invention describes the high-concentration preparation of
 CC soluble thrombomodulin. The present sequence represents a human soluble
 CC thrombomodulin, which is given in the exemplification of the present
 CC invention.
 XX SQ Sequence 516 AA;
 Query Match 100.0%; Score 2830; DB 7; Length 516;
 Best Local Similarity 100.0%; Pred. No. 7.5e-150;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISLLNGD 60
 DB 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISLLNGD 78
 QY 61 GGVGRRRLWTGLQPPCGGPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 DB 79 GGVGRRRLWTGLQPPCGGPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPTWEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAVSIYGTFFA 180
 DB 139 AVSAAEATVPSEPTWEQCEVKADGFLCEPHFPATCRPLAVEPGAAAAVSIYGTFFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 240
 DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGEHCNA 258
 QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVPNPDPQPGSYSCMCETGYRLAA 300
 DB 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVPNPDPQPGSYSCMCETGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPCPCQRCVNTQGGFCHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
 DB 319 DQHRCEVDVDCILEPSPCPCQRCVNTQGGFCHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 378

QY	361	QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCCEPGYILDDGFI	420
DB	379	QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCCEPGYILDDGFI	438
QY	421	CTDIDECENGFCGSGVCHNLPTFFECICGPOSALARHIGTDCDSKVDGSGSGSGEPSPS	480
DB	439	CTDIDECENGFCGSGVCHNLPTFFECICGPOSALARHIGTDCDSKVDGSGSGSGEPSPS	498
QY	481	PTPGSTLTTPPAVLVHSG 498	
DB	499	PTPGSTLTTPPAVLVHSG 516	
RESULT 5			
ID	ABG72575	standard; protein; 575 AA.	
XX	AC	ABG72575;	
XX	DT	05-MAR-2003 (first entry)	
XX	XX	Human thrombomodulin protein #2 (CD141).	
XX	XX	Human; thrombomodulin; CD141; dendritic cell separation; inflammation;	
XX	KW	antiinflammatory; cytostatic; antiarthritic; antirheumatic;	
XX	KW	immunosuppressive; dermatological; cell therapy; dermatomyositis; cancer;	
XX	KW	autoimmune disorder; rheumatoid arthritis; psoriatic arthritis;	
XX	KW	alkylosing spondylitis; Sjorgen's syndrome; lupus erythematosus;	
XX	KW	Goodpasture's syndrome; scleroderma; vasculitis; polymyositis.	
XX	OS	Homo sapiens.	
XX	XX	WO200293172-A1.	
XX	PD	21-NOV-2002.	
XX	PF	17-MAY-2002; 2002WO-US015786.	
XX	PT	17-MAY-2001; 2001US-0291561P.	
XX	PR	(MILT-) MILTENYI BIOTEC INC.	
XX	PI	Schmitz J, Dziunek A, Buck DW;	
XX	PI	WPI; 2003-129324/12.	
XX	PT	Enriching for dendritic cells from a mixture of cells, useful for	
XX	PT	treating inflammation, cancer or autoimmune disorders such as arthritis,	
XX	PT	or lupus by contacting the mixture of cell with an antigen-binding	
XX	PT	fragment specific for CD141.	
XX	PS	Example 1; Fig 3B; 88pp; English.	
XX	CC	This invention relates to a novel method for separating dendritic cells	
XX	CC	from a mixture of cells. The method comprises contacting the mixture of	
XX	CC	cells with an antigen-binding fragment specific for CD141, and selecting	
XX	CC	the cells that are CD141 positive therefore producing a dendritic cell-	
XX	CC	enriched composition. The method of the invention may have	
XX	CC	antiinflammatory; cytostatic; antiarthritic; antirheumatic;	
XX	CC	immunosuppressive and dermatological activities and may be used in cell	
XX	CC	therapy. The methods, compositions and agents of the invention are useful	
XX	CC	for treating inflammation, cancer or autoimmune disorders such as	
XX	CC	rheumatoid arthritis, psoriatic arthritis, alkylosing spondylitis,	
XX	CC	Sjorgen's syndrome, lupus erythematosus, Goodpasture's syndrome,	
XX	CC	scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic	
XX	CC	cells and populations are useful for screening assays for agents that	
XX	CC	affect dendritic cell function, and for the phenotypic, functional,	
XX	CC	biochemical or molecular analyses of dendritic cells. The compositions	
XX	CC	and dendritic cells are useful as vaccine adjuvants. The present sequence	
XX	CC	represents a protein sequence of human CD141 protein which is used to	
XX	CC	generate the dendritic cell specific antibodies that are used in the	
XX	CC	method of the invention	

XX	SQ	Sequence 575 AA;	
QY	Query Match	100.0%; Score 2830; DB 6; Length 575;	
DB	Best Local Similarity	100.0%; Pred. No. 8.3e-150;	
QY	Matches 498; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
DB	1	APASPPQGGSCVCHDHFALYFGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	60
DB	19	APAEPPQGGSCVCHDHFALYFGPATFLNASQICDGLRGHLMTVRSSVAADVISLLNGD	78
QY	61	GGVGRRLWIGLQPLPPGCGDKRIGLPIRGFQWVTGDNNTSYSRWARLDINGAPLCPLCV	120
DB	79	GGVGRRLWIGLQPLPPGCGDKRIGLPIRGFQWVTGDNNTSYSRWARLDINGAPLCPLCV	138
QY	121	AVSAAEATVPSEPIWEEQOCEVKADGFLCEFFPATCRPLAVEPGAAAAAASITYGTTPA	180
DB	139	AVSAAEATVPSEPIWEEQOCEVKADGFLCEFFPATCRPLAVEPGAAAAAASITYGTTPA	198
QY	181	ARGADFOALPVGSSAAVAFGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA	240
DB	199	ARGADFOALPVGSSAAVAFGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA	258
QY	241	IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA	300
DB	259	IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA	318
QY	301	DOHRCEDVDDCILEPSPCPQRCVNTQGGFECHCYPNYDLVDGECVEPDPFRANCEYQC	360
DB	319	DOHRCEDVDDCILEPSPCPQRCVNTQGGFECHCYPNYDLVDGECVEPDPFRANCEYQC	378
QY	361	QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCCEPGYILDDGFI	420
DB	379	QPLNQTSLVCAEGFAPIPHEPHRCQMFQNTACPADCDNTQASCCEPGYILDDGFI	438
QY	421	CTDIDECENGFCGSGVCHNLPTFFECICGPOSALARHIGTDCDSKVDGSGSGEPSPS	480
DB	439	CTDIDECENGFCGSGVCHNLPTFFECICGPOSALARHIGTDCDSKVDGSGSGEPSPS	498
QY	481	PTPGSTLTTPPAVLVHSG 498	
DB	499	PTPGSTLTTPPAVLVHSG 516	
RESULT 6			
ID	ABM78950	standard; protein; 575 AA.	
XX	AC	ABM78950;	
XX	AC	ABM78950;	
DT	15-JAN-2004	(first entry)	
XX	XX	Breast cancer specific marker under-expressed in breast cancer.	
XX	XX	Breast cancer; marker; thrombomodulin; human; diagnosis; cytostatic;	
XX	XX	biochip; vaccine.	
OS	XX	Homo sapiens.	
XX	XX	WO2003073911-A2.	
PN	12-SEP-2003.		
PD	27-FEB-2003; 2003WO-US005984.		
XX	28-FEB-2002; 2002US-0359999P.		
XX	(GEO) UNIV GEORGETOWN.		
XX	Su YA, Yang J;		
PI	WPI; 2003-721995/68.		
DR	N-PSDB; ACF79930.		

XX PT Detecting breast cancer in a subject comprises contacting a biological
 PT sample with an agent that binds to a polynucleotide or polypeptide of a
 XX breast-cancer specific gene (BCSG).
 XX
 XX Claim 5; Page 119-121; 143pp; English.
 XX
 XX The present sequence is that of a breast cancer specific marker (BCSM)
 CC encoded by a gene identified by microarray gene expression analysis as
 CC being under-expressed in breast cancers in comparison to healthy tissue.
 CC The BCSM was identified as thrombomodulin (THBD), a negative regulator of
 CC coagulation previously reported to be involved in vascular diseases and
 CC cancers. It is 1 of 19 (see ABW78941-59) BCSMs of the invention that are
 CC encoded by breast cancer specific genes (BCSGs) which are differentially
 CC expressed in breast cancer cell lines and breast cancer tissue samples as
 CC compared to control cell lines and normal tissue samples. The invention
 CC provides a method for detection of breast cancer by measuring expression
 CC levels of BCSGs, and in particular the level of polynucleotides
 CC transcribed from and polypeptides encoded by the BCSGs. A pharmaceutical
 CC composition for the treatment of breast cancer comprises a BCSM, an
 CC antibody directed against a BCSM, a vaccine generated using a BCSM, or an
 CC agent that modulates an expression level of a BCSG or an activity of a
 CC BCSM. A biochip for diagnosing breast cancer or screening agents that
 CC inhibit breast cancer comprises a BCSG or BCSM
 XX Sequence 575 AA;

Query Match 100.0%; Score 2830; DB 7; Length 575;
 Best Local Similarity 100.0%; Pred. No. 8.3e-150;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 78
 QY 61 GGVRRLWIGLQPLPGCGDPKRLGRLGFWQWTDGNTSYSRWARLDLNGAPLCGLCV 120
 Db 79 GGVRRLWIGLQPLPGCGDPKRLGRLGFWQWTDGNTSYSRWARLDLNGAPLCGLCV 138
 QY 121 AVSAAEATVPEPIWEQCEVADGFLCEFHFPATCRPLAVEPGAAAVSITVGTFFA 180
 Db 139 AVSAAEATVPEPIWEQCEVADGFLCEFHFPATCRPLAVEPGAAAVSITVGTFFA 198
 QY 181 ARGADFQALPVGSSAAVAPLGLQMLCTAPPVAGVQGHWAREAPGAMDCSVENGCCHEA 240
 Db 199 ARGADFQALPVGSSAAVAPLGLQMLCTAPPVAGVQGHWAREAPGAMDCSVENGCCHEA 258
 QY 241 IPGAPRCOCAPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQSGYSCMCTGVRLAA 300
 Db 259 IPGAPRCOCAPAGALQADGSCSTASATQSCNDLCEHFVCPNPDQSGYSCMCTGVRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQPCQVNTQGGFECHCYPNYDLVDGCEVPDPFCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCQVNTQGGFECHCYPNYDLVDGCEVPDPFCFRANCEYQC 378
 QY 361 QPLNQTSLVCARGFAPIEPHRCQMFNQTACADCPNTQASCEPGEVILDDGFI 420
 Db 379 QPLNQTSLVCARGFAPIEPHRCQMFNQTACADCPNTQASCEPGEVILDDGFI 438
 QY 421 CTDIDECNGGFCGVCNHLPGTTEFCICGPDPSALAHIGTDCDSKVGQDGSGEPPPS 480
 Db 439 CTDIDECNGGFCGVCNHLPGTTEFCICGPDPSALAHIGTDCDSKVGQDGSGEPPPS 498
 QY 481 PTFGSLTPPAVLVHSG 498
 Db 499 PTFGSLTPPAVLVHSG 516
 RESULT 7
 ID ADE54760
 XX ADE54760 standard; protein; 575 AA.
 AC ADE54760;

XX DT 29-JAN-2004 (first entry)
 XX Human Protein P07204, SEQ ID NO 565.
 DE
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS WO2003016475-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 FI MPI; 2003-268312/26.
 XX GENBANK; P07204.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/publiished_pct_sequences.
 XX
 SQ Sequence 575 AA;

Query Match 100.0%; Score 2830; DB 7; Length 575;
 Best Local Similarity 100.0%; Pred. No. 8.3e-150;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVHDCFCALYPGPATFLNASQICDGLRGLHMTVRSSVAADVLSLLNGD 78
 QY 61 GGVRRLWIGLQPLPGCGDPKRLGRLGFWQWTDGNTSYSRWARLDLNGAPLCGLCV 120

derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published/pct_sequences.

XX Sequence 575 AA;
S0

```
Query Match      100.0%; Score 2830; DB 7; Length 575;
Best Local Similarity 100.0%; Pred. No. 3.e-150;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	APAEPPGSGSCVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD	60
Db			
QY	19	APAEPPGSGSCVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD	78
Db			
QY	61	GGVGRRLWIGLQLPFGCGDKPKRGLGPLRGFWQTGDNNTSYSRWARLDLNGAPLCGPLCV	120
Db			
QY	79	GGVGRRLWIGLQLPFGCGDKPKRGLGPLRGFWQTGDNNTSYSRWARLDLNGAPLCGPLCV	138
Db			
QY	121	AVSAEAATVPSPPIWEEOCEVKADGFICEPHFPATCEPLAVEPGAAAAAASITYGTFFA	180
Db			
QY	139	AVSAEAATVPSPPIWEEOCEVKADGFICEPHFPATCEPLAVEPGAAAAAASITYGTFFA	198
Db			
QY	181	ARGADFQALPVGSSAAVALPLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGECHACNA	240
Db			
QY	199	ARGADFQALPVGSSAAVALPLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGECHACNA	258
Db			
QY	241	IPGAPRCQCAGAAALQADGRSCTASTATQSCNDLCEHF CVPNPDPQSGYSVMCETGYRLAA	300
Db			
QY	259	IPGAPRCQCAGAAALQADGRSCTASTATQSCNDLCEHF CVPNPDPQSGYSVMCETGYRLAA	318
Db			
QY	301	DQHRCEVDVCILPEPSCPQR CVNTQGFECHCYPNYDLVDGECPEVPDPCFRANCEYCQC	360
Db			
QY	319	DQHRCEVDVCILPEPSCPQR CVNTQGFECHCYPNYDLVDGECPEVPDPCFRANCEYCQC	378
Db			
QY	361	QPLNQTSYLVCABGFAP I PHEPRCFMFCNQ TACPADC DPNTQASCEPEGVIILDDGI	420
Db			
QY	379	QPLNQTSYLVCABGFAP I PHEPRCFMFCNQ TACPADC DPNTQASCEPEGVIILDDGI	438
Db			
QY	421	CTDIDECENGFCGCVGNLP LGTFECCICGPD SALARIHGITDCDSKVG DGDGSGSGGPPPS	480
Db			
QY	439	CTDIDECENGFCGCVGNLP LGTFECCICGPD SALARIHGITDCDSKVG DGDGSGSGGPPPS	498
Db			
QY	481	PTPGSTLTTPPAVLVHSG	498
Db			
QY	499	PTPGSTLTTPPAVLVHSG	516
Db			

RESULT 9
ABG72572
ID ABG72572 standard; protein; 631 AA.
XX

db	79	GGVGRRLWIGLQPPGCCDPKXELPLRGFWVTGDNNTSYSRWARLDLNGAPLQCP	138
QY	121	AVSAAEATVPSEPIWESQCEVKADGFLCEFHFPATCRPLAVEPGAAAASVITGTTPA	180
db	139	AVSAAEATVPSEPIWESQCEVKADGFLCEFHFPATCRPLAVEPGAAAASVITGTTPA	198
QY	181	ARGADFQALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVENGGECHACNA	240
db	199	ARGADFQALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVENGGECHACNA	258
QY	241	IPGAPRCQCPAGAAIQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSQMCSTGRLAA	300
db	259	IPGAPRCQCPAGAAIQADGRSCTASATQSCNDLCEHFCVNPDPQGSYSQMCSTGRLAA	318
QY	301	DOHRCEDVDDCILEPSPQRCVNTQGGFECHCPNTDLDGECVEVPDPCFRANCEYQC	360
db	319	DOHRCEDVDDCILEPSPQRCVNTQGGFECHCPNTDLDGECVEVPDPCFRANCEYQC	378
QY	361	QPLNQTSYLCVCAEGFAPIPHEPHECMFCNQTACPADCDPNTQASCCEPGYILDDGFI	420
db	379	QPLNQTSYLCVCAEGFAPIPHEPHECMFCNQTACPADCDPNTQASCCEPGYILDDGFI	438
db	401	QPLNQTSYLCVCAEGFAPIPHEPHECMFCNQTACPADCDPNTQASCCEPGYILDDGFI	460

421 CTTDCECGGFCGVCNHLPGTFECICGPD SARHIGTDCDSKVDGDSGSGGEPPPS 498

Dd
Qy
Db

481 PTEGSTLTTPAVGLVHSG 498
| | | | |
499 PTEGSTLTTPAVGLVHSG 516

XX	RESULT 8
XX	ADD48168
XX	ID ADD48168 standard; protein; 575 AA.
XX	AC ADD48168;
XX	29-JAN-2004 (first entry)
XX	Human Protein NP_000352, SEQ ID NO 13866.
XX	Human; pain; neuronal tissue; gene therapy;
XX	spinal segmental nerve injury; chronic constriction injury; CCI;
XX	spared nerve injury; SNI; Chung.
XX	Homo sapiens.
XX	WO2003016475-A2.
XX	27-FEB-2003.
XX	14-AUG-2002; 2002WO-US025765.
XX	14-AUG-2001; 2001US-0312147P.
XX	01-NOV-2001; 2001US-0346382P.
XX	26-NOV-2001; 2001US-033347P.
XX	(GEO) GEN HOSPITAL CORP.
XX	(FARB) BAYER AG.
XX	Woolf C, D'urso D, Befort K, Costigan M;
XX	WPI; 2003-268312/26.
XX	GENBANK; NP_000352.
XX	New composition comprising two or more isolated polypeptides, useful for
XX	preparing a medicament for treating pain in an animal.
XX	Claim 1; Page; 1017pp; English.
XX	The invention discloses a composition comprising two or more isolated rat
XX	protein fragments.

CC or human polynucleotides or a polynucleotide which represents a fragment

AC ABG72572;
 XX 05-MAR-2003 (first entry)
 XX Human thrombomodulin protein #1 (CD141).
 XX Human; thrombomodulin; CD141; dendritic cell separation; inflammation;
 KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; cell therapy; dermatomyositis; cancer;
 KW autoimmune disorder; rheumatoid arthritis; psoriatic arthritis;
 KW alkylating spondylitis; Sjorgen's syndrome; lupus erythematosus;
 KW Goodpasture's syndrome; scleroderma; vasculitis; polymyositis.
 XX
 OS Homo sapiens.
 XX
 XX WO200293172-A1.
 XX
 XX 21-NOV-2002.
 XX
 XX 17-MAY-2002; 2002WO-US015786.
 XX
 XX 17-MAY-2001; 2001US-0291561P.
 XX
 XX (MILT-) MILTENYI BIOTEC INC.
 XX
 XX Schmitz J, Dzionek A, Buck DW;
 XX WPI; 2003-129324/12.
 XX
 XX Enriching for dendritic cells from a mixture of cells, useful for
 PT treating inflammation, cancer or autoimmune disorders such as arthritis,
 PT or lupus by contacting the mixture of cell with an antigen-binding
 PT fragment specific for CD141.
 XX
 XX Example 1; Fig 3A; 88pp; English.
 XX
 CC This invention relates to a novel method for separating dendritic cells
 CC from a mixture of cells. The method comprises contacting the mixture of
 CC cells with an antigen-binding fragment specific for CD141, and selecting
 CC the cells that are CD141 positive therefore producing a dendritic cell-
 CC enriched composition. The method of the invention may have
 CC antiinflammatory; cytostatic; antiarthritic; antirheumatic;
 CC immunosuppressive and dermatological activities and may be used in cell
 CC therapy. The methods, compositions and agents of the invention are useful
 CC for treating inflammation, cancer or autoimmune disorders such as
 CC rheumatoid arthritis, psoriatic arthritis, alkylating spondylitis,
 CC Sjorgen's syndrome, lupus erythematosus, Goodpasture's syndrome,
 CC scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic
 CC cells and populations are useful for screening assays for agents that
 CC affect dendritic cell function, and for the phenotypic, functional,
 CC biochemical or molecular analyses of dendritic cells. The compositions
 CC and dendritic cells are useful as vaccine adjuvants. The present sequence
 CC represents a protein sequence of human CD141 protein which is used to
 CC generate the dendritic cell specific antibodies that are used in the
 CC method of the invention
 XX
 SQ Sequence 631 AA;
 Query Match 100.0%; Score 2830; DB 6; Length 631;
 Best Local Similarity 100.0%; Pred. NO. 9e-150;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVHDCFALYFGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 60
 DB 75 APAEPQGGSCQVHDCFALYFGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 134
 QY 61 GGVGRRRLWIGLQPLPGCGDKPRGLRGLRGQWVTGDMNTYSRWABLDLNGAPLCPCLV 120
 DB 135 GGVGRRRLWIGLQPLPGCGDKPRGLRGLRGQWVTGDMNTYSRWABLDLNGAPLCPCLV 194
 QY 121 AVSAAEATVPSEPIWEEQCEKADGFLCEFHFPATCRPLAVEPGAAAASVITVTGTPA 180
 DB 195 AVSAAEATVPSEPIWEEQCEKADGFLCEFHFPATCRPLAVEPGAAAASVITVTGTPA 254

QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSVENGCGEHACNA 240
 DB 255 ARGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSVENGCGEHACNA 314
 QY 241 IGAERCCOCPAGALOADGRSCTASATQSCNDLCEHFCVNPDPQSGYSQMCETGYELAA 300
 DB 315 IGAERCCOCPAGALOADGRSCTASATQSCNDLCEHFCVNPDPQSGYSQMCETGYELAA 374
 QY 301 DQHRCEVDVDDCILPEPSPQRCVNTQGGFCHCYPNVDLVGECVFPVDFCFRANCEYQC 360
 DB 375 DQHRCEVDVDDCILPEPSPQRCVNTQGGFCHCYPNVDLVGECVFPVDFCFRANCEYQC 434
 QY 361 QPLNOTSILVCVCAEGFAPIPHEHRCQMFNCTACPADCDPNTQASCECEGVILDDGFI 420
 DB 435 QPLNOTSILVCVCAEGFAPIPHEHRCQMFNCTACPADCDPNTQASCECEGVILDDGFI 494
 QY 421 CTDIDECENGFCGCVCHNLPGTFECICGPDLSALRHIGTDCDSKGVGDSGSGFPFPPS 480
 DB 495 CTDIDECENGFCGCVCHNLPGTFECICGPDLSALRHIGTDCDSKGVGDSGSGFPFPPS 554
 QY 481 PTPGSTLTPPAVGLVHSG 498
 DB 555 PTPGSTLTPPAVGLVHSG 572
 RESULT 10
 AAR84185
 ID AAR84185 standard; protein; 498 AA.
 XX
 AC AAR84185;
 XX
 DI 05-JUN-1996 (first entry)
 XX
 DE Human derived thrombomodulin.
 XX
 KW Human thrombomodulin; hepatopathy; fulminant hepatitis.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 349..463
 FT /note= "fragment AAR84184"
 XX
 PN WO9528953-A1.
 XX
 PD 02-NOV-1995.
 XX
 PF 10-APR-1995; 95WO-JP000704.
 XX
 PR 20-APR-1994; 94JP-00081196.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Fujiwara K, Mochida S;
 XX
 DR WPI; 1995-302844/49.
 XX
 XX Hepatopathy treatment pref. comprising human derived thrombomodulin -
 PT useful against, e.g, fulminant hepatitis.
 XX
 PS Claim 2; Page 17-20; 29pp; Japanese.
 XX
 CC The human derived thrombomodulin AAR84185, and its fragment AAR84184 can
 CC be used in the treatment of hepatopathy, including fulminant hepatitis
 XX
 SQ Sequence 498 AA;
 Query Match 99.9%; Score 2826; DB 2; Length 498;
 Best Local Similarity 99.8%; Pred. NO. 1.2e-149;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APAEPQGGSCQVHDCFALYFGPATFLNASQICDGLRGLHMTVRSSVAADVISLLNGD 60

Db 1 APAEPQPGSGQCVHEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGFGFOWTGDNNNTSYSRWARLDNGAPLCGPLCV 120
Db 61 GGVGRRRLWIGLQLPFGCGDPKRLGFGFOWTGDNNNTSYSRWARLDNGAPLCGPLCV 120
QY 121 AVSAAEATVPSEPIWEQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 121 AVSAAEATVPSEPIWEQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
QY 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHAACNA 240
Db 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHAACNA 240
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAA 300
Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAA 300
QY 301 DQHRCEVDVDCILLEPSPCPORCVNTQGGFECHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
Db 301 DQHRCEVDVDCILLEPSPCPORCVNTQGGFECHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCOMFCNOTACPADCDPNTQASCCEPGYILDDGFI 420
Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCOMFCNOTACPADCDPNTQASCCEPGYILDDGFI 420
QY 421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALAHIGHITDCCDQSGKVDGSGSGGEPSPS 480
Db 421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALAHIGHITDCCDQSGKVDGSGSGGEPSPS 480
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 481 PTPGSTLTTPPAVGLVHSG 498

RESULT 11
AAW01600
ID AAW01600 standard; protein; 498 AA.
XX AAW01600;
XX 17-MAR-1997 (first entry)
XX Thrombomodulin TWE456 protein.
XX Thrombomodulin; nervous interference; treatment; medulla injury.
XX Homo sapiens.
XX JP08283174-A.
XX 29-OCT-1995.
XX 11-APR-1995; 95JP-00085202.
XX 11-APR-1995; 95JP-00085202.
XX (ASAH) ASAH KASEI KOGYO KK.
XX WPI; 1997-017314/02.
XX Treating agent for nervous interference after medulla injury - contains
XX thrombomodulin as active component.
XX Claim 2; Page 5-6; 6pp; Japanese.

AAW01599-600 are fragments of human thrombomodulin. They can be used in
treatment of nervous interference after medulla injury. In an example, a
model of medulla injury was prep. by compressing a male Wistar rat of
200-250 g body wt., with a 20g weight for 20 mins. TMD123 dissolved in
physiological saline water was injected into the tail vein 30 mins.
before injury. Movement function was evaluated 24 hrs. after injury. MPO

CC activity in medulla tissue was measured 3 hrs. after injury as an index
CC of neutrophile accumulation. The Tarlov score was 1.50 compared to 0.77
CC for the control, and complete paralysis was 15.4 percent compared to 35.3
CC percent for the control
XX Sequence 498 AA;
SQ
Query Match 99.9%; Score 2826; DB 2; Length 498;
Best Local Similarity 99.8%; Pred. No. 1.2e-149;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 APAEPQPGSGQCVHEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
Db 1 APAEPQPGSGQCVHEHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGFGFOWTGDNNNTSYSRWARLDNGAPLCGPLCV 120
Db 61 GGVGRRRLWIGLQLPFGCGDPKRLGFGFOWTGDNNNTSYSRWARLDNGAPLCGPLCV 120
QY 121 AVSAAEATVPSEPIWEQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 121 AVSAAEATVPSEPIWEQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPFA 180
QY 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHAACNA 240
Db 181 ARGADFQALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGCGEHAACNA 240
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAA 300
Db 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAA 300
QY 301 DQHRCEVDVDCILLEPSPCPORCVNTQGGFECHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
Db 301 DQHRCEVDVDCILLEPSPCPORCVNTQGGFECHCYPNYDLVDGCEVPEVDPFCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCOMFCNOTACPADCDPNTQASCCEPGYILDDGFI 420
Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCOMFCNOTACPADCDPNTQASCCEPGYILDDGFI 420
QY 421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALAHIGHITDCCDQSGKVDGSGSGGEPSPS 480
Db 421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALAHIGHITDCCDQSGKVDGSGSGGEPSPS 480
QY 481 PTPGSTLTTPPAVGLVHSG 498
Db 481 PTPGSTLTTPPAVGLVHSG 498
RESULT 12
AAV67402
ID AAV67402 standard; protein; 498 AA.
XX AAV67402;
XX 12-MAY-2000 (first entry)
XX Novel sugar chain-bonded thrombomodulin-like peptide #2.
XX Thrombomodulin; sugar chain; thrombin; coagulation; protein C; DIC;
XX anticoagulant; blood coagulation disorder; heart muscle; brain; liver;
XX disseminated intravenous coagulation; peripheral blood vessel sclerosis;
XX kidney infarction; toxemia; pregnancy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Key Misc-difference 455
XX FT /label= Val or Ala
XX PN WC200000516-A1.
XX PD 06-JAN-2000.
XX

PF 30-JUN-1999; 99WC-JP003532.
 XX
 PR 30-JUN-1998; 98JP-00199654.
 XX
 PA (MOCH) MOCHIDA PHARM CO LTD.
 XX
 PI Hase S, Wakabayashi H;
 XX
 DR WPI; 2000-160668/14.
 XX
 XX
 PT Sugar chain-bound thrombomodulin-like peptide, for treatment of, e.g.
 PT disseminated intravenous coagulation.
 XX
 XX
 PS Claim 2; Page 35-37; 40pp; Japanese.
 XX
 XX The invention provides a thrombomodulin-like peptide bearing a glucuronic
 CC acid(betal-3)galactose(betal-3)galactose(betal-4)xylose sugar chain
 CC sulfated at the 3-position. The peptide binds to anti-human natural
 CC killer cell 1 antibody. It also binds to thrombin, inhibiting coagulation
 CC and promoting protein C activation. The peptide may be used as an
 CC anticoagulant for the treatment of blood coagulation disorders.
 CC disseminated intravenous coagulation (DIC), peripheral blood vessel
 CC sclerosis, heart muscle, brain, liver or kidney infarction, and toxemia
 CC of pregnancy. The peptide has low toxicity. The present sequence
 CC represents a novel thrombomodulin-like peptide sequence
 XX
 XX Sequence 498 AA;
 SQ
 Query Match 99.9%; Score 2826; DB 3; Length 498;
 Best Local Similarity 99.8%; Pred. No. 1.2e-149;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 APAEPQGGSCQVHDCPFLYPGPATFLNASQICDGLRGHLMTVRSVAADVLSILLNGD 60
 Db 1 APAEPQGGSCQVHDCPFLYPGPATFLNASQICDGLRGHLMTVRSVAADVLSILLNGD 60
 Qy 61 GGVRRRLWIGLQLPPGCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 Db 61 GGVRRRLWIGLQLPPGCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 Qy 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPA 180
 Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPA 180
 Qy 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
 Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
 Qy 241 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCEGYRLAA 300
 Db 241 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCEGYRLAA 300
 Qy 301 DQHRCEVDVDCILEPSPCQPCQVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Db 301 DQHRCEVDVDCILEPSPCQPCQVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Qy 361 QPLNQTSYLCVCAEGFAPIPHEPHRCMFCNOTACPADCDPNTQASCECPGYLLDDGFI 420
 Db 361 QPLNQTSYLCVCAEGFAPIPHEPHRCMFCNOTACPADCDPNTQASCECPGYLLDDGFI 420
 Qy 421 CTDIDECENGFGCGVCHNLPGTFECICGPDGALAHRIHTDCCDCKVDGSDSGSGEPSPS 480
 Db 421 CTDIDECENGFGCGVCHNLPGTFECICGPDGALAHRIHTDCCDCKVDGSDSGSGEPSPS 480
 Qy 481 PTPGSTLTTPAVGLVHSG 498
 Db 481 PTPGSTLTTPAVGLVHSG 498
 RESULT 13
 AAR22016
 ID AAR22016 standard; protein; 516 AA.
 XX

AC AAR22016;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-JUL-1992 (first entry)
 XX
 XX Truncated human thrombomodulin encoded by plasmid pSV2TMD1.
 DE
 XX Thrombin binding site; blood clotting; TMD1 deleter.
 XX
 OS Homo sapiens.
 XX
 PN EP474273-A.
 XX
 PD 11-MAR-1992.
 XX
 PF 05-AUG-1991; 91EP-00202009.
 XX
 PR 03-AUG-1990; 90JP-00204978.
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX Zushi M, Gomi K, Yamamoto S, Suzuki K, Matsuda A;
 PI
 XX WPI; 1992-081820/11.
 DR
 XX New polypeptide inhibits blood coagulation and platelet aggregation -
 PT promotes thrombin catalysed protein C activation for treating myocardial
 PT infarction, thrombosis, embolism, etc.
 PT
 XX Example 1; Page 17; 112pp; English.
 PS
 XX Plasmid M13mp19TMJ3 (see AAR22013) was used as template for site-directed
 CC mutagenesis. A 177bp fragment was deleted using the "TMD1 deleter" -
 CC oligonucleotide to give plasmid M13TMD1 which encodes the first 516 N-
 CC terminal amino acids of human thrombomodulin. Plasmid M13TMD1 was
 CC completely digested with HindIII and BamHI and a TMD1 fragment of ca.
 CC 1700bp was isolated. The fragment was ligated to HindIII- and BglII-cut
 CC plasmid pSV2-dhfr to give the recombinant plasmid pSV2TMD1. See AAR22014-
 CC R22022 and AAQ25072. (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 516 AA;
 Query Match 99.9%; Score 2826; DB 2; Length 516;
 Best Local Similarity 99.8%; Pred. No. 1.3e-149;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 APAEPQGGSCQVHDCPFLYPGPATFLNASQICDGLRGHLMTVRSVAADVLSILLNGD 60
 Db 19 APAEPQGGSCQVHDCPFLYPGPATFLNASQICDGLRGHLMTVRSVAADVLSILLNGD 78
 Qy 61 GGVRRRLWIGLQLPPGCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 Db 79 GGVRRRLWIGLQLPPGCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
 Qy 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPA 180
 Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSIYGTTPA 198
 Qy 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 258
 Qy 241 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCEGYRLAA 300
 Db 259 IPGAPRCOCAGALQADGRSCTASATQSCNDLCEHFCVNPDPQSGSYSCMCEGYRLAA 318
 Qy 301 DQHRCEVDVDCILEPSPCQPCQVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPCQPCQVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 378
 Qy 361 QPLNQTSYLCVCAEGFAPIPHEPHRCMFCNOTACPADCDPNTQASCECPGYLLDDGFI 420
 Db 379 QPLNQTSYLCVCAEGFAPIPHEPHRCMFCNOTACPADCDPNTQASCECPGYLLDDGFI 438

QY 421 CTDIDECENGFCGVCNHLPGTFFECICGPDALAHIGTDCDCKVVDGDSGSGEPPPS 480
 Db 439 CTDIDECENGFCGVCNHLPGTFFECICGPDALAHIGTDCDCKVVDGDSGSGEPPPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 14
 AAY09347
 ID AAY09347 standard; protein; 516 AA.
 AC AAY09347;
 XX
 DT 08-JUL-1999 (first entry)
 DE Human thrombomodulin SEQ ID NO:1.
 KW Human; thrombomodulin; aqueous parenteral solution; storage; diabetes.
 KW distribution; acute coronary syndrome; thrombosis; embolism; diabetes.
 OS Homo sapiens.
 XX
 PN WO9918994-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 13-OCT-1998; 98WO-JP004609.
 XX
 PR 15-OCT-1997; 97JP-00281659.
 PR 11-NOV-1997; 97JP-00308523.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Yui M, Yokozawa A, Murata T, Tsuruta K, Shimizu H;
 XX
 DR WPI; 1999-277444/23.
 DR N-PSDB; AAX55879.
 XX
 PT Stable aqueous parenteral thrombomodulin solution - comprising buffer and
 PT surfactant, useful for treating acute coronary syndrome, thrombosis,
 PT embolism, and diabetes.
 PS Claim 6; Page 87-89; 97pp; Japanese.

The present invention describes a method for maintaining the quality of
 an aqueous parenteral solution of thrombomodulin comprising buffer and
 surfactant aseptically filled in a case or syringe. Maintaining the
 quality of an aqueous, parenteral thrombomodulin solution is
 characterised in that the solution: (a) comprises soluble thrombomodulin,
 a buffer to maintain the pH at 5-7 and a surfactant; (b) is aseptically
 filled into: (i) a case or (ii) a syringe without any empty space; and
 (c) is kept in liquid form in storage and distribution and not frozen or
 freeze dried. Thrombomodulin is used to treat acute coronary syndrome
 (such as myocardial infarction, unstable angina and coronary artery
 blockage), thrombosis (e.g. cerebral, vascular and peripheral blood
 vessel thrombosis), embolism, peripheral blood vessel disorders (e.g.
 Raynaud's disease), arteriosclerosis, vasculitis (e.g. due to systemic
 lupus erythematosus or Barrett's syndrome), multiple organ failure,
 disseminated intravascular coagulation, transient ischaemia, diabetes,
 liver veno-occlusive diseases and deep vein thrombosis. The composition
 is stable for a long period of time and can be stored and distributed in
 ready to use form avoiding the problems of dissolution and accuracy when
 preparing on demand. The present sequence represents human thrombomodulin

Query Match 99.9%; Score 2826; DB 2; Length 516;
 Best Local Similarity 99.8%; Pred. No. 1.3e-149;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAPQPGSCQVEHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAADVISLLNGD 60
 Db 19 APAPQPGSCQVEHDCFALYPGPATFLNASQICDGLRHLMTVRSSVAADVISLLNGD 78
 QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFGQWVTGDNNTSYSRWRLDINGAPLCGLVCV 120
 Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFGQWVTGDNNTSYSRWRLDINGAPLCGLVCV 138
 QY 121 AVSAAEATVPSEPIWEEQQCEVKADGFLCEFFHPATCRPLAVEPFGAAAAVITYGTPTA 180
 Db 139 AVSAAEATVPSEPIWEEQQCEVKADGFLCEFFHPATCRPLAVEPFGAAAAVITYGTPTA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
 Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
 QY 301 DOHRCEDVDDCILEPSPCPORCVNTQGGFECHCYPNVLDVDCGCEVPDPFCFRANCEYQC 360
 Db 319 DOHRCEDVDDCILEPSPCPORCVNTQGGFECHCYPNVLDVDCGCEVPDPFCFRANCEYQC 378
 QY 361 QPLNQTSLVCAEGPAPIPHEHRCQMFNCQTACADCPNTOASCEGFIIDDGFI 420
 Db 379 QPLNQTSLVCAEGPAPIPHEHRCQMFNCQTACADCPNTOASCEGFIIDDGFI 438
 QY 421 CTDIDECENGFCGVCNHLPGTFFECICGPDALAHIGTDCDCKVVDGDSGSGEPPPS 480
 Db 439 CTDIDECENGFCGVCNHLPGTFFECICGPDALAHIGTDCDCKVVDGDSGSGEPPPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 15
 AAY83934
 ID AAY83934 standard; protein; 516 AA.
 XX
 AC AAY83934;
 XX
 DT 28-JUL-2000 (first entry)
 DE Human thrombomodulin TMD protein.
 DE
 KW Human; thrombomodulin; vasculitis; protein C; thrombin.
 OS Homo sapiens.
 XX
 PN JP2000053582-A.
 XX
 PD 22-FEB-2000.
 XX
 PF 06-AUG-1998; 98JP-00222688.
 XX
 PR 06-AUG-1998; 98JP-00222688.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-353249/31.
 DR N-PSDB; AAA10027.
 XX
 PT Treating agent for vasculitis contains peptide which promotes activation
 PT of protein C by thrombin.
 XX
 PS Claim 4; Page 10-12; 18pp; Japanese.
 XX
 CC This sequence represents a human thrombomodulin protein. The invention
 CC relates to a treating agent for vasculitis containing a peptide which
 CC promotes activation of protein C by thrombin
 XX

SQ Sequence 516 AA;
Query Match 99.9%; Score 2826; DB 3; Length 516;
Best Local Similarity 99.8%; Pred. No. 1.3e-149;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	APAEPOGSGQVEHDCFALYGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD	60
Db	19	APAEPOGSGQVEHDCFALYGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD	78
Qy	61	GGVRRRLWIGLQPLPGCGDKRLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV	120
Db	79	GGVRRRLWIGLQPLPGCGDKRLGLRGPQWVTGDNNTSYSRWARLDLNGAPLCGLCV	138
Qy	121	AVSAEATVPSEPIWEEQCEVKADGFLCEHFPATCEPLAVEPGAAAAVSITYGTPEA	180
Db	139	AVSAEATVPSEPIWEEQCEVKADGFLCEHFPATCEPLAVEPGAAAAVSITYGTPEA	198
Qy	181	ARGADFOALFVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA	240
Db	199	ARGADFOALFVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA	258
Qy	241	IPGAPRCQCPAGAAQADGRSCTASATOSCNLCEHFCVNPDPQSGYSWCETGYRLAA	300
Db	259	IPGAPRCQCPAGAAQADGRSCTASATOSCNLCEHFCVNPDPQSGYSWCETGYRLAA	318
Qy	301	DQHRCEVDVDCILESPQPCQRCVNTQGGFECHYCNVNDLVGECVEPVDFCFRANCEYQC	360
Db	319	DQHRCEVDVDCILESPQPCQRCVNTQGGFECHYCNVNDLVGECVEPVDFCFRANCEYQC	378
Qy	361	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQACQACPADCDPNTQASCECEGYLDDGFI	420
Db	379	QPLNQTSYLCVCAEGFAPIPHEPHRCQMFQACQACPADCDPNTQASCECEGYLDDGFI	438
Qy	421	CTDIDECENGCGFCGVCHNLPGTFECICGPDALAHIGTCDGKVDGDSGSGGEPPPS	480
Db	439	CTDIDECENGCGFCGVCHNLPGTFECICGPDALAHIGTCDGKVDGDSGSGGEPPPS	498
Qy	481	PTFGSTLTTPPAVGLVHSG	498
Db	499	PTFGSTLTTPPAVGLVHSG	516

Search completed: June 9, 2004, 08:47:58
Job time : 54.5 secs

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:46:09 ; Search time 16.5 Seconds
(without alignments)
1558.166 Million cell updates/sec

Title: US-09-509-994-2_COPY_19_516

Perfect score: 2830
Sequence: 1 APABPQPGSQVCHDFAL.....PSPTPGSTLTPPAVLGHSG 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCFUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2830	100.0	575	1	US-08-312-870-1
2	2830	100.0	575	6	5466668-6
3	2826	99.9	498	2	US-08-733-564-2
4	2826	99.9	575	1	US-08-261-206A-59
5	2826	99.9	575	4	US-09-880-484D-2
6	2824	98.8	497	1	US-08-312-870-3
7	2822	99.7	575	1	US-08-170-290A-54
8	2820	99.6	497	4	US-09-331-793-4
9	2760.5	97.5	572	6	5256770-7
10	2680	94.7	476	1	US-08-014-723-1
11	2680	94.7	476	1	US-08-110-011A-1
12	2680	94.7	494	1	US-08-014-723-14
13	2680	94.7	494	1	US-08-110-011A-14
14	2678	94.6	476	1	US-08-014-723-2
15	2678	94.6	476	1	US-08-014-723-18
16	2678	94.6	476	1	US-08-110-011A-2
17	2678	94.6	476	1	US-08-110-011A-18
18	2678	94.6	494	1	US-08-014-723-16
19	2678	94.6	494	1	US-08-110-011A-16
20	2604	92.0	475	1	US-08-307-444A-2
21	2604	92.0	475	1	US-08-587-389-2
22	2600	91.9	475	1	US-08-307-444A-1
23	2600	91.9	475	1	US-08-587-389-1
24	2596	91.7	456	1	US-08-307-444A-4
25	2596	91.7	456	1	US-08-587-389-4
26	2592	91.6	456	1	US-08-307-444A-3
27	2592	91.6	456	1	US-08-587-389-3

28	2543	89.9	446	1	US-08-307-444A-5	Sequence 5, Appli
29	2543	89.9	446	1	US-08-587-389-5	Sequence 5, Appli
30	1621	57.3	275	1	US-08-312-870-7	Sequence 7, Appli
31	1159	41.0	215	1	US-08-312-870-5	Sequence 5, Appli
32	689	24.3	115	1	US-08-312-870-9	Sequence 9, Appli
33	681	24.1	114	2	US-08-733-564-1	Sequence 1, Appli
34	579	20.5	652	2	US-08-751-305-2	Sequence 2, Appli
35	566.5	20.0	492	4	US-09-724-864-39	Sequence 39, Appli
36	356	12.6	638	2	US-08-897-443-1	Sequence 1, Appli
37	352	12.4	58	1	US-08-261-206A-3	Sequence 3, Appli
38	348.5	12.3	915	4	US-09-507-794A-34	Sequence 34, Appli
39	348.5	12.3	915	4	US-09-905-125A-34	Sequence 34, Appli
40	348.5	12.3	915	4	US-09-902-775A-34	Sequence 34, Appli
41	334.5	11.8	1964	4	US-09-467-997-1	Sequence 1, Appli
42	326.5	11.5	956	2	US-08-897-443-3	Sequence 3, Appli
43	323	11.4	1253	3	US-08-479-722B-4	Sequence 4, Appli
44	322.5	11.4	1394	6	5177197-30	Patent No. 5177197
45	321	11.3	2321	4	US-09-230-652-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-06-312-870-1
; Sequence 1, Application US/08312870
; Patent No. 5639625
; GENERAL INFORMATION:
; APPLICANT: Carson, Craig W.
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Method for Detecting Antibodies to
; Thrombomodulin in Patients
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/312,870
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansen, Eugenia S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: OMRF B35150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 19..575
US-08-312-870-1

Query Match 100.0%; Score 2830; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 7.5e-193;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 60
DB 19 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGCGDKRILGRLGFWGTGDNNTSYSRWRLDNLGAPLCPLCV 120
DB 79 GGVGRRRLWIGLQPLPGCGDKRILGRLGFWGTGDNNTSYSRWRLDNLGAPLCPLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEFGAAAAVSIYGTGPPA 180
DB 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEFGAAAAVSIYGTGPPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAREAPGAWDCSVENGGEHACNA 240
DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAREAPGAWDCSVENGGEHACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
QY 301 DOHRCEDVDCLLESPCPQRCVNTQGGFECHCYPNYDLVDGECVPEVDPCEFRANCEYOC 360
DB 319 DOHRCEDVDCLLESPCPQRCVNTQGGFECHCYPNYDLVDGECVPEVDPCEFRANCEYOC 378
QY 361 OPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECEGYILDDGFI 420
DB 379 OPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECEGYILDDGFI 438
QY 421 CTDIDECENGFCVCHNLPGTFECICGPDLSALARIHGTDCDSKVDGSGSGSEPPPS 480
DB 439 CTDIDECENGFCVCHNLPGTFECICGPDLSALARIHGTDCDSKVDGSGSGSEPPPS 498
QY 481 PTFGSTLTTPPAVGLVHSG 498
DB 499 PTFGSTLTTPPAVGLVHSG 516

RESULT 2
546668-6
; Patent No. 546668
; APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT, DAVID R.
; TITLE OF INVENTION: SUPERIOR THROMBOMODULIN ANALOGS FOR PHARMACEUTICAL USE
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; FILING DATE: 22-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 568,456
; FILING DATE: 15-AUG-1990
; APPLICATION NUMBER: 506,325
; FILING DATE: 09-APR-1990
; APPLICATION NUMBER: 406,941
; FILING DATE: 13-SEP-1989
; APPLICATION NUMBER: 345,374
; FILING DATE: 28-APR-1989
; SEQ ID NO: 6:
; LENGTH: 575
546668-6

Query Match 100.0%; Score 2830; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 7.5e-193;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 60
DB 19 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGCGDKRILGRLGFWGTGDNNTSYSRWRLDNLGAPLCPLCV 120
DB 79 GGVGRRRLWIGLQPLPGCGDKRILGRLGFWGTGDNNTSYSRWRLDNLGAPLCPLCV 138

QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEFGAAAAVSIYGTGPPA 180
DB 139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEFGAAAAVSIYGTGPPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAREAPGAWDCSVENGGEHACNA 240
DB 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVOGHWAREAPGAWDCSVENGGEHACNA 258
QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
QY 301 DOHRCEDVDCLLESPCPQRCVNTQGGFECHCYPNYDLVDGECVPEVDPCEFRANCEYOC 360
DB 319 DOHRCEDVDCLLESPCPQRCVNTQGGFECHCYPNYDLVDGECVPEVDPCEFRANCEYOC 378
QY 361 OPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECEGYILDDGFI 420
DB 379 OPLNQTSYLCVCAEGFAPIPHEPHRCQMFNCQTACPADCDPNTQASCECEGYILDDGFI 438
QY 421 CTDIDECENGFCVCHNLPGTFECICGPDLSALARIHGTDCDSKVDGSGSGSEPPPS 480
DB 439 CTDIDECENGFCVCHNLPGTFECICGPDLSALARIHGTDCDSKVDGSGSGSEPPPS 498
QY 481 PTFGSTLTTPPAVGLVHSG 498
DB 499 PTFGSTLTTPPAVGLVHSG 516

RESULT 3
US-08-733-564-2
; Sequence 2, Application US/08733564
; Patent No. 5916874
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, Kenji
; APPLICANT: MOCHIDA, Satoshi
; TITLE OF INVENTION: METHOD FOR TREATING LIVER INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,564
; FILING DATE: 18 OCTOBER 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 0216-0362P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-733-564-2

Query Match 99.9%; Score 2826; DB 2; Length 498;
Best Local Similarity 99.8%; Pred. No. 1.2e-192;

Wed Jun 9 13:16:02 2004

Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 APAEPQPGSQCVHDCFALYPGATFLNASQICDGLRGLHMTVRSSVAADVISILLNGD 60

1 APAEPQPGSQCVHDCFALYPGATFLNASQICDGLRGLHMTVRSSVAADVISILLNGD 60

61 GGVGRRRLWIGLQPLPGGDKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 120

61 GGVGRRRLWIGLQPLPGGDKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 120

121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHPFATCRPLAVEPGAAAASVITYGTFFA 180

121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHPFATCRPLAVEPGAAAASVITYGTFFA 180

181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHACNA 240

181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHACNA 240

241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300

241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300

301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFECHCYPNYDLVDGCEVPDPCFRANCEYQC 360

301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFECHCYPNYDLVDGCEVPDPCFRANCEYQC 360

361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCEPEGYILDDGFI 420

361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCEPEGYILDDGFI 420

421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALRHIGTDCDVGKVDGSGSGGEPSPS 480

421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALRHIGTDCDVGKVDGSGSGGEPSPS 480

481 PTPGSTLTTPPAVGLVHSG 498

481 PTPGSTLTTPPAVGLVHSG 498

RESULT 4

US-08-261-206A-59

Sequence 59, Application US/08261206A

Patent No. 5574007

GENERAL INFORMATION:

APPLICANT: Zushi, Mitichitaka

APPLICANT: Gomi, Komakazu

APPLICANT: Yamamoto, Shuji

APPLICANT: Suzuki, Koji

APPLICANT: Matsuoka, Akio

TITLE OF INVENTION: A polypeptide Capable of Interacting

TITLE OF INVENTION: with Thrombin

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 N. Washington St.

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22046-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261,206A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/740,492

FILING DATE: 03-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 216-275P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300

TELEFAX: 703-241-2848

TELEX: 248345

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 575 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Protein

LOCATION: 1-575

OTHER INFORMATION: /label= protein

OTHER INFORMATION: /note= "human thrombomodulin"

US-08-261-206A-59

Query Match 99.9%; Score 2826; DB 1; Length 575;

Best Local Similarity 99.8%; Pred. No. 1.4e-192; Indels 0; Gaps 0;

Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 APAEPQPGSQCVHDCFALYPGATFLNASQICDGLRGLHMTVRSSVAADVISILLNGD 60

19 APAEPQPGSQCVHDCFALYPGATFLNASQICDGLRGLHMTVRSSVAADVISILLNGD 78

61 GGVGRRRLWIGLQPLPGGDKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 120

79 GGVGRRRLWIGLQPLPGGDKRLGLPLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 138

121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHPFATCRPLAVEPGAAAASVITYGTFFA 180

139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHPFATCRPLAVEPGAAAASVITYGTFFA 198

181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHACNA 240

199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHACNA 258

241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300

259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 318

301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFECHCYPNYDLVDGCEVPDPCFRANCEYQC 360

319 DQHRCEVDVDCILEPSPQPCORCVNTQGGFECHCYPNYDLVDGCEVPDPCFRANCEYQC 378

361 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCEPEGYILDDGFI 420

379 QPLNQTSYLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCEPEGYILDDGFI 438

421 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALRHIGTDCDVGKVDGSGSGGEPSPS 480

439 CTDIDECENGFCGVCCHNLPGTFECICGPDSSALRHIGTDCDVGKVDGSGSGGEPSPS 498

481 PTPGSTLTTPPAVGLVHSG 498

499 PTPGSTLTTPPAVGLVHSG 516

RESULT 5

US-09-880-484D-2

Sequence 2, Application US/09880484D

Patent No. 6632791

GENERAL INFORMATION:

APPLICANT: Light, David

APPLICANT: Nagashima, Mariko

APPLICANT: Morser, Michael J

TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use

FILE REFERENCE: 51863AUSM1

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,870
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-870-3

Query Match 99.8%; Score 2824; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APAEPQGGSCVQVHDCFALYPGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
Db 1 APAEPQGGSCVQVHDCFALYPGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
QY 61 GGVRRRLMIGLQIPGCGDPEKLGRLGFQWVTGDNNTSYSRWARLDLNGAPLGLCV 120
Db 61 GGVRRRLMIGLQIPGCGDPEKLGRLGFQWVTGDNNTSYSRWARLDLNGAPLGLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCFHFPPATCRPLAVEPGAAAAVSYTGTPFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCFHFPPATCRPLAVEPGAAAAVSYTGTPFA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVNGGCEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVNGGCEHACNA 240
QY 241 IPGAPROCCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGYSYCMCTGYRLAA 300
Db 241 IPGAPROCCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGYSYCMCTGYRLAA 300
QY 301 DOHRCEDVDDCILPEPSPQPCVNTQGGFCHCPVNDLVGECVPEVDPFCFRANCEYQC 360
Db 301 DOHRCEDVDDCILPEPSPQPCVNTQGGFCHCPVNDLVGECVPEVDPFCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCTACPADCDNTQASCCEPGYILLDDGFI 420
Db 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCTACPADCDNTQASCCEPGYILLDDGFI 420
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARIHGTDCDCKVDDGSGSGSEPPPS 480
Db 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARIHGTDCDCKVDDGSGSGSEPPPS 480
QY 481 PTPGSTLTTPPAVGLVHS 497
Db 481 PTPGSTLTTPPAVGLVHS 497

RESULT 7
US-08-170-290A-54
; Sequence 54, Application US/08170290A
; Patent No. 5702931
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Morser, Michael J.
; APPLICANT: Zielander, Laura R.
; TITLE OF INVENTION: No. 5702931el Mutagenesis Methods and
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 63

QY 1 APAEPQGGSCVQVHDCFALYPGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
Db 19 APAEPQGGSCVQVHDCFALYPGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 78
QY 61 GGVRRRLMIGLQIPGCGDPEKLGRLGFQWVTGDNNTSYSRWARLDLNGAPLGLCV 120
Db 79 GGVRRRLMIGLQIPGCGDPEKLGRLGFQWVTGDNNTSYSRWARLDLNGAPLGLCV 138
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCFHFPPATCRPLAVEPGAAAAVSYTGTPFA 180
Db 139 AVSAAEATVPSEPIWEEQCEVKADGFLCFHFPPATCRPLAVEPGAAAAVSYTGTPFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVNGGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHWAREAPGAWDCSVNGGCEHACNA 258
QY 241 IPGAPROCCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGYSYCMCTGYRLAA 300
Db 259 IPGAPROCCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGYSYCMCTGYRLAA 318
QY 301 DOHRCEDVDDCILPEPSPQPCVNTQGGFCHCPVNDLVGECVPEVDPFCFRANCEYQC 360
Db 319 DOHRCEDVDDCILPEPSPQPCVNTQGGFCHCPVNDLVGECVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCTACPADCDNTQASCCEPGYILLDDGFI 420
Db 379 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCTACPADCDNTQASCCEPGYILLDDGFI 438
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARIHGTDCDCKVDDGSGSGSEPPPS 480
Db 439 CTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARIHGTDCDCKVDDGSGSGSEPPPS 498
QY 481 PTPGSTLTTPPAVGLVHS 498
Db 499 PTPGSTLTTPPAVGLVHS 516

RESULT 6
US-08-312-870-3
; Sequence 3, Application US/08312870
; Patent No. 5639625
; GENERAL INFORMATION:
; APPLICANT: Carson, Craig W.
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Method for Detecting Antibodies to
; TITLE OF INVENTION: Thrombomodulin in Patients
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James M. Heslin
;; STREET: 379 Lytton Ave.
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/170,290A
;; FILING DATE: 28-DEC-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/05573
;; FILING DATE: 01-JUL-1992
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/724,237
;; FILING DATE: 01-JUL-1991
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heslin, James M.
;; REGISTRATION NUMBER: 29,541
;; REFERENCE/DOCKET NUMBER: 11972-58-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 54:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 575 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-170-290A-54

Query Match 99.7%; Score 2822; DB 1; Length 575;
Best Local Similarity 99.8%; Pred. No. 2.8e-192;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
DB 19 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 78
QY 61 GGVGRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGPLCV 120
DB 79 GGVGRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGPLCV 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPA 180
DB 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
DB 199 ARGADFOALPVGSSAAVAPLGLQMTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 258
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 259 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
QY 301 DQHRCEVDVDCILEPSPQRCVNTQGGFCHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
DB 319 DQHRCEVDVDCILEPSPQRCVNTQGGFCHCYPNYDLVDGECVEPVPDPCFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCNOTACPADCPNTQASCECEGYLLDDGFI 420
DB 379 QPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCNOTACPADCPNTQASCECEGYLLDDGFI 438
QY 421 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALAHIGTDCDCKVGDGSGSGEPPPS 480

DB 439 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALAHIGTDCDCKVGDGSGSGEPPPS 498
QY 481 PTPGSTLTTPPAVGLVHSG 498
DB 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 8
US-09-331-793-4
; Sequence 4, Application US/09331793
; Patent No. 6500646
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/09/331,793
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-331-793-4

Query Match 99.6%; Score 2820; DB 4; Length 497;
Best Local Similarity 99.8%; Pred. No. 3.3e-192;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
DB 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGHLMTVSSVAADVLSLLNGD 60
QY 61 GGVGRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGPLCV 120
DB 61 GGVGRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGPLCV 120
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPA 180
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEFHFPATCRPLAVEPGAAAAVSIYGTTPA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQMTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
DB 181 ARGADFOALPVGSSAAVAPLGLQMTAPPGAVQGHWAREAPGAWDCSVENGCEHACNA 240
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
DB 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
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DB 421 CTDIDECENGFCGVCVCHNLPGTFECICGPDSSALAHIGTDCDCKVGDGSGSGEPPPS 480
QY 481 PTPGSTLTTPPAVGLVHSG 497
DB 481 PTPGSTLTTPPAVGLVHSG 497

RESULT 9
5256770-7
; Patent No. 5256770
; APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
; DAVID R.
; TITLE OF INVENTION: OXIDATION RESISTANT THROMBOMODULIN ANALOGS

Wed Jun 9 13:16:02 2004

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/014,723

FILING DATE: 19930208

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5273962man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 80-071-0 CIP

TELEPHONE: (703)413-3000

TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-014-723-1

Query Match 94.7%; Score 2680; DB 1; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.6e-182;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 60
Db 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 60
QY 61 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 120
Db 61 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
QY 241 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
Db 241 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
QY 301 DQHRCEVDVDCILPEPSPQPCORCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
Db 301 DQHRCEVDVDCILPEPSPQPCORCVNTQGGFECHCYPNYDLVDGECVEPVDPCFRANCEYQC 360
QY 361 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCNOTACPADCDPNTQASCECEGYILDDGFI 420
Db 361 QPLNQTSLYLCVCAEGFAPIPHEHRCQMFNCNOTACPADCDPNTQASCECEGYILDDGFI 420
QY 421 CTDIDECENGFCGVCNHLPGTFECICGPDLSALRHIGTDCSGKVDGSDSGEPPPS 476
Db 421 CTDIDECENGFCGVCNHLPGTFECICGPDLSALRHIGTDCSGKVDGSDSGEPPPS 476

```

RESULT 11
US-08-110-011A-1
; Sequence 1, Application US/08110011A
; Patent No. 5354664

GENERAL INFORMATION:

APPLICANT: Doi, Takeshi

APPLICANT: Iwasaki, Akio

APPLICANT: Saino, Yushi

APPLICANT: Kimura, Shigeru

APPLICANT: Ohkuchi, Masao

TITLE OF INVENTION: Thrombin-Binding Substance and Process

TITLE OF INVENTION: For Preparing the Same

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

NUMBER OF SEQUENCES: 48

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/506,325

FILING DATE: 09-APR-1990

SEQ ID NO: 7

LENGTH: 572

5256770-7

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Query Match 97.5%; Score 2760.5; DB 6; Length 572;
Best Local Similarity 98.6%; Pred. No. 6.2e-188;
Matches 491; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 60
Db 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 60
QY 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 78
Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGLHMTVRSVAADVLSLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 120
Db 61 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 120
QY 79 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 137
Db 79 GGVGRRRLWIGLQPLPGGDKPKRLGFLRGFWVTGDNNTSYSRWARLDINGAPLCGLCV 137
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 180
QY 138 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 197
Db 138 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTTPFA 197
QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSVENGGEHACNA 240
QY 198 ARGADFOALPVGSSAAVAPLGLQLMCTA--GNVQGHWAREAPGAWDCSVENGGEHACNA 255
Db 198 ARGADFOALPVGSSAAVAPLGLQLMCTA--GNVQGHWAREAPGAWDCSVENGGEHACNA 255
QY 241 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
Db 241 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
QY 256 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 315
Db 256 IPGAPRCQCPAGAAQADGSCCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 315
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QY 496 PTPGSTLTTPRAVGLVHSG 513
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RESULT 10
US-08-014-723-1
; Sequence 1, Application US/08014723
; Patent No. 5273962

GENERAL INFORMATION:

APPLICANT: Doi, Takeshi

APPLICANT: Iwasaki, Akio

APPLICANT: Saino, Yushi

APPLICANT: Kimura, Shigeru

APPLICANT: Ohkuchi, Masao

TITLE OF INVENTION: Thrombin-Binding Substance and Process

TITLE OF INVENTION: For Preparing the Same

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

Wed Jun 9 13:16:02 2004

ADDRESSEE: P.C. Jefferson Davis Highway, Fourth Floor
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-073-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-110-011A-1

Query Match 94.7%; Score 2680; DB 1; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.6e-182;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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1 APAEPQPGSQCVHDCFPALPGPATFLNASQICDGLRGLMTVRSSVAADVLSILLNGD 60
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RESULT 12
US-08-014-723-14
Sequence 14, Application US/08014723
Patent No. 5273962
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi

Query Match 94.7%; Score 2680; DB 1; Length 494;
Best Local Similarity 99.2%; Pred. No. 2.7e-182;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 319 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYFNYDLVDGECVDFPCFRANCEYQC 378
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Db 379 QPLNQTSLYCVCAEGFAPIPHEPHRCQMFNCNQACPADCDPNTQASCECEGYILDDGFI 438
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Db 439 CTDIDECENGFCGVCNHLPGTFECICGPDALSARHIGTDCDSKVDGSGSGSE 494

RESULT 14

US-08-014-723-2
; Sequence 2, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-014-723-2

Query Match 94.6%; Score 2678; DB 1; Length 476;
Best Local Similarity 98.9%; Pred. No. 3.6e-182;
Matches 471; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAAVSITYGTTPFA 180
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RESULT 13

US-08-110-011A-14
; Sequence 14, Application US/08110011A
; Patent No. 5354664
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,011A
; FILING DATE: 23-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5354664man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-073-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-011A-14

Query Match 94.7%; Score 2680; DB 1; Length 494;
Best Local Similarity 99.2%; Pred. No. 2.7e-182;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 APAEPQPGSGSCVHDCFCALYPGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 60
Db 1 APAEPQPGSGSCVHDCFCALYPGPATFLNASQICDGLRGHLMTVSRSSVAADVLSLLNGD 78
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Qy 301 DQHRCEVDVDCILEPSPQRCVNTQGGFECHCYFNYDLVDGECVDFPCFRANCEYQC 360

Query Match 94.6%; Score 2678; DB 1; Length 476;
Best Local Similarity 99.2%; Pred. No. 3.6e-182;
Matches 471; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAWDCSVENGCGEHACNA 240
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RESULT 15
US-08-014-723-18
Sequence 18, Application US/08014723
Patent No. 5273962

GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 469
OTHER INFORMATION: /note= "acidic amino acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 470
OTHER INFORMATION: /note= "acidic amino acid"

Wed Jun 9 13:16:02 2004

GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2826	99.9	575	US-09-938-405-2	Sequence 2, Appl
5	2826	99.9	575	US-09-880-464-2	Sequence 2, Appl
6	2826	99.9	575	US-10-438-648-2	Sequence 2, Appl
7	2826	99.9	575	US-10-410-195-2	Sequence 4, Appl
8	2820	99.6	497	US-10-298-796-4	Sequence 196, Appl
9	2819	99.6	575	US-10-094-886-196	Sequence 2759, Ap
10	1032	36.5	239	US-10-104-047-2759	Sequence 2, Appl
11	735	26.0	418	US-10-427-805-3	Sequence 3, Appl
12	715	25.3	397	US-10-427-805-3	Sequence 3, Appl
13	582	20.6	645	US-10-029-386-33151	Sequence 3151, A
14	582	20.6	652	US-10-408-765A-1422	Sequence 1422, Ap
15	580	20.5	652	US-09-789-919-96	Sequence 96, Appl

Sequence 131, Appl
Sequence 83, Appl
Sequence 176, Appl
Sequence 177, Appl
Sequence 196, Appl
Sequence 107, Appl
Sequence 190, Appl
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Sequence 73, Appl
Sequence 77, Appl
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Sequence 195, Appl
Sequence 21, Appl
Sequence 102, Appl
Sequence 1187, Ap
Sequence 176, Appl
Sequence 1292, Ap

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43	357	12.6	741	16	US-10-408-765A-1187
44	357	12.6	782	12	US-10-428-275-176
45	357	12.6	794	11	US-09-833-245-1292

ALIGNMENTS

RESULT 1
US-10-150-440-3
; Sequence 3, Application US/10150440
; Publication No. US20030022249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Juergen
; APPLICANT: Buzek, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; TITLE OF INVENTION: A SUBSET OF DENDRITIC CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 212302001200
; CURRENT APPLICATION NUMBER: US/10/150,440
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-3

Query Match 100.0%; Score 2830; DB 14; Length 575;

Wed Jun 9 13:16:02 2004

Best Local Similarity 100.0%; Pred. No. 3.9e-193; Indels 0; Gaps 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
19 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 78
61 GGVGRRRLWIGLQPLPPGGDPKRLGFLRGFOWTGDNNNTSRSRWALDLNAPLCGLCV 120
79 GGVGRRRLWIGLQPLPPGGDPKRLGFLRGFOWTGDNNNTSRSRWALDLNAPLCGLCV 138
121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITGTFFA 180
139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITGTFFA 198
181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAVQGHWAREAPGAWDCSVENGCGEHCNA 240
199 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAVQGHWAREAPGAWDCSVENGCGEHCNA 258
241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 300
259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCETGYRLAA 318
301 DOHRCEDVDDCILEPSPCPORCVNTQGFECCHCYPNYDLVDGECVBPVDFCFRANCEYQC 360
319 DOHRCEDVDDCILEPSPCPORCVNTQGFECCHCYPNYDLVDGECVBPVDFCFRANCEYQC 378
361 QPLNQTSLVLCVACAGFAPIPHEHRCQMFNQTACPADCDPNTQASCECEGYILDDGFI 420
379 QPLNQTSLVLCVACAGFAPIPHEHRCQMFNQTACPADCDPNTQASCECEGYILDDGFI 438
421 CTTDIDECENGFCGVCNHLPGTFECICGPDALAHIGTDCDCKVGDGSGSGEPPPS 480
439 CTTDIDECENGFCGVCNHLPGTFECICGPDALAHIGTDCDCKVGDGSGSGEPPPS 498
481 PTPGSTLTTPPAVGLVHSG 498
499 PTPGSTLTTPPAVGLVHSG 516

RESULT 3

US-10-150-440-1
; Sequence 1, Application US/10150440
; Publication No. US2003002249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Juergen
; APPLICANT: Dzonek, Andrej
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; FILE REFERENCE: 212302001200
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-1

Query Match 100.0%; Score 2830; DB 14; Length 631;
Best Local Similarity 100.0%; Pred. No. 4.3e-193;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
75 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 134
61 GGVGRRRLWIGLQPLPPGGDPKRLGFLRGFOWTGDNNNTSRSRWALDLNAPLCGLCV 120

RESULT 2

US-10-373-801-29
; Sequence 29, Application US/10373801
; Publication No. US20040005644A1
; GENERAL INFORMATION:
; APPLICANT: Yibai Pharmaceutical (USA)
; TITLE OF INVENTION: Method and composition for detection and treatment of breast can
; FILE REFERENCE: 12399.00
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 29
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-801-29

Query Match 100.0%; Score 2830; DB 15; Length 575;
Best Local Similarity 100.0%; Pred. No. 3.9e-193;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 60
19 APAPQPGGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVLSLLNGD 78
61 GGVGRRRLWIGLQPLPPGGDPKRLGFLRGFOWTGDNNNTSRSRWALDLNAPLCGLCV 120
79 GGVGRRRLWIGLQPLPPGGDPKRLGFLRGFOWTGDNNNTSRSRWALDLNAPLCGLCV 138
121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITGTFFA 180
139 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITGTFFA 198

Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 378
 QY 361 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 420
 Db 379 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 438
 QY 421 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALAHIGTDCDSKVDGSDSGSGEPSPS 480
 Db 439 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALAHIGTDCDSKVDGSDSGSGEPSPS 498
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 5
 US-09-880-464-2
 ; Sequence 2, Application US/09880464
 ; Publication No. US20030011623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morser, Michael J
 ; APPLICANT: Nagashima, Mariko
 ; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
 ; FILE REFERENCE: Improved Thrombomodulin Analogs
 ; CURRENT APPLICATION NUMBER: US/09/880,464
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR FILING DATE: 2000-06-21
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 575
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-880-464-2

Query Match 99.9%; Score 2826; DB 10; Length 575;
 Best Local Similarity 99.8%; Pred. No. 7.5e-193;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD 78
 QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGFLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGFLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 180
 Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 300
 Db 259 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 318
 QY 301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 360
 Db 319 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 378
 QY 361 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 420
 Db 379 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 438

Db 135 GGVGRRRLWIGLQPLPGCGDPKRLGFLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 194
 QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 180
 Db 195 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 254
 QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 240
 Db 255 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 314
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 300
 Db 315 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 374
 QY 301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 360
 Db 375 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVDPVPCFRANCEYQC 434
 QY 361 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 420
 Db 435 QPLNQTSLVCAEGFAPIPHEPHRCQMFQNOTACPADCDNTQASCECPGYILDDGFI 494
 QY 421 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALAHIGTDCDSKVDGSDSGSGEPSPS 480
 Db 495 CTDIDCEGNGFCGVCNHLPGTFECICGPDSSALAHIGTDCDSKVDGSDSGSGEPSPS 554
 QY 481 PTPGSTLTTPPAVGLVHSG 498
 Db 555 PTPGSTLTTPPAVGLVHSG 572

RESULT 4
 US-09-938-405-2
 ; Sequence 2, Application US/09938405
 ; Patent No. US20020111296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pestoff, Barry W.
 ; APPLICANT: Morser, Michael J.
 ; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
 ; FILE REFERENCE: 51960AUSM1
 ; CURRENT APPLICATION NUMBER: US/09/938,405
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 60/229,714
 ; PRIOR FILING DATE: 2000-08-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 575
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-938-405-2

Query Match 99.9%; Score 2826; DB 9; Length 575;
 Best Local Similarity 99.8%; Pred. No. 7.5e-193;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD 60
 Db 19 APAEPQGGSCQVEHDCFALYPGPATFLNASQICDGLRGHLMTVRSVAADVLSLLNGD 78
 QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGFLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
 Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGFLRGFWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
 QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 180
 Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFHPCATPLAVEPGAAAAAASITYGTPFA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 240
 Db 199 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGGEHACNA 258
 QY 241 IPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEGYRLAA 300

Wed Jun 9 13:16:02 2004

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421 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 480
439 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 498
481 PTPGSTLTTPPAVLVHSG 498
499 PTPGSTLTTPPAVLVHSG 516

RESULT 6
US-10-438-648-2
; Sequence 2, Application US/10438648
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagaehima, Mariko
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSD1
; CURRENT APPLICATION NUMBER: US/10/438,648
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 60/213,678
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/880,484
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-438-648-2

Query Match 99.9%; Score 2826; DB 14; Length 575;
Best Local Similarity 99.8%; Pred. No. 7.5e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 60
Db 19 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 258
QY 241 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 300
Db 259 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 318
QY 301 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 360
Db 319 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 420
Db 379 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 438
QY 421 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 480
Db 439 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 498
QY 481 PTPGSTLTTPPAVLVHSG 498
Db 499 PTPGSTLTTPPAVLVHSG 516

US-10-438-648-2
; Sequence 2, Application US/10438648
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagaehima, Mariko
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSD1
; CURRENT APPLICATION NUMBER: US/10/438,648
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 60/213,678
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/880,484
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-438-648-2

Query Match 99.9%; Score 2826; DB 14; Length 575;
Best Local Similarity 99.8%; Pred. No. 7.5e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 60
Db 19 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 258
QY 241 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 300
Db 259 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 318
QY 301 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 360
Db 319 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 420
Db 379 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 438
QY 421 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 480
Db 439 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 498
QY 481 PTPGSTLTTPPAVLVHSG 498
Db 499 PTPGSTLTTPPAVLVHSG 516

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RESULT 7
US-10-410-195-2
; Sequence 2, Application US/10410195
; Publication No. US20040002446A1
; GENERAL INFORMATION:
; APPLICANT: Pestoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/10/410,195
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US/09/938,405
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-195-2

Query Match 99.9%; Score 2826; DB 15; Length 575;
Best Local Similarity 99.8%; Pred. No. 7.5e-193;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 60
Db 19 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGLMTVRSVAADVISLLNGD 78
QY 61 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 120
Db 79 GGVGRRRLWIGLQPLPGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCGLCV 138
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 180
Db 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFFPATCRPLAVEPGAAAAVSIYGTFFA 198
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 240
Db 199 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCGCEHACNA 258
QY 241 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 300
Db 259 IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCEYGLAA 318
QY 301 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 360
Db 319 DQHRCEVDVDCILEPSPQPCQVCNTQGGFECHCYPNYDLVDGECVPEVDPFCFRANCEYQC 378
QY 361 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 420
Db 379 QPLNQTSLYLCVCAEGFAPLIPHEPHRCQMFNCOTACPADCDPNTQASCEPGEYILDGFI 438
QY 421 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 480
Db 439 CTIDECENGFCGCVCHNLPGTFFCICGPDALAHIGTDCDSKVDGSGSGGSEPPPS 498
QY 481 PTPGSTLTTPPAVLVHSG 498
Db 499 PTPGSTLTTPPAVLVHSG 516

RESULT 8
US-10-298-796-4
; Sequence 4, Application US/10298796
; Publication No. US2003020490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi

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Wed Jun 9 13:16:02 2004

; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-4

Query Match 99.6%; Score 2820; DB 15; Length 497;
Best Local Similarity 99.8%; Pred. No. 1.7e-192;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGLHMTVRSSVAADVVISLLNGD 60
Db 1 APAEPQGGSCQVEHDCFALYGPATFLNASQICDGLRGLHMTVRSSVAADVVISLLNGD 60
QY 61 GGVGRRRLWIGLQPPGCGDKPLRGFQWVTGDNNTSYSRWRLDNGAPLCPGLCV 120
Db 61 GGVGRRRLWIGLQPPGCGDKPLRGFQWVTGDNNTSYSRWRLDNGAPLCPGLCV 120
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAASVITYGTTPA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAASVITYGTTPA 180
QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAASVITYGTTPA 180
Db 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAASVITYGTTPA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
QY 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
Db 181 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAGVQGHWAREAPGAWDCSVENGCEHACNA 240
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
Db 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
Db 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
QY 301 DOHRCEDVDDCILBPSPCQPCVNTQSGFECHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
Db 301 DOHRCEDVDDCILBPSPCQPCVNTQSGFECHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
QY 301 DOHRCEDVDDCILBPSPCQPCVNTQSGFECHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
Db 301 DOHRCEDVDDCILBPSPCQPCVNTQSGFECHCYPNYDLVDGECVEPVPDPCFRANCEYQC 360
QY 361 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQACPADCDNTQASCCEPGEYLLDDGFI 420
Db 361 QPLNQTSYLCVCAEGFAPIPHEPHRCOMFCNQACPADCDNTQASCCEPGEYLLDDGFI 420
QY 421 CTDIIDECENGFCGVCNHLPGTFECICGPDSEALRHIGTDCDCKGVDDGSDSGSGEPSPS 480
Db 421 CTDIIDECENGFCGVCNHLPGTFECICGPDSEALRHIGTDCDCKGVDDGSDSGSGEPSPS 480
QY 481 PTPGSTLTTPPAVLVHS 497
Db 481 PTPGSTLTTPPAVLVHS 497

RESULT 9
US-10-094-886-196
; Sequence 196, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Keskuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Sytek, Kimberly A.
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh

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301 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVPEVDFCFRANCEYQC 360
 319 DQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVPEVDFCFRANCEYQC 378
 361 OPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNQTACPADCDNTOASCCEPGYILDDGFI 420
 379 OPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNQTACPADCDNTOASCCEPGYILDDGFI 438
 421 CTDIDECENGFCSCGVCHNLPGTFECICGPDALAHIGTDCDCKVDGSGSGEPPPS 480
 439 CTDIDECENGFCSCGVCHNLPGTFECICGPDALAHIGTDCDCKVDGSGSGEPPPS 498
 481 PTPGSTLTTPPAVGLVHSG 498
 499 PTPGSTLTTPPAVGLVHSG 516

RESULT 10
 US-10-104-047-2759
 ; Sequence 2759, Application US/10104047
 ; Publication No. US2003023632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McLean, Kirk
 ; TITLE OF INVENTION: HELIX RESEARCH INSTITUTE
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2759
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-2759
 Query Match 36.5%; Score 1032; DB 15; Length 239;
 Best Local Similarity 86.1%; Pred. No. 1.2e-65;
 Matches 179; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
 291 MCETGYRLAADQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVPEVDF 350
 1 MCETGYRLAADQHRCEVDVDCILEPSPQPCORCVNTQGGFCHCYPNYDLVDGECVPEVDF 60
 351 CFRANCEYOCQPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNQTACPADCDNTOASCCEP 410
 61 CFRANCEYOCQPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNQTACPADCDNTOASCCE-- 118
 411 EGYILDDGFICTDIDECENGFCSCGVCHNLPGTFECICGPDALAHIGTDCDCKVDGSG 470
 119 -----CHNLPGTFECICGPDALAHIGTDCDCKVDGSG 152
 471 DSGSGEPPPSPTPGSTLTTPPAVGLVHSG 498
 153 DSGSGEPPPSPTPGSTLTTPPAVGLVHSG 180

RESULT 11
 US-10-427-805-2
 ; Sequence 2, Application US/10427805
 ; Publication No. US20040063632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McLean, Kirk
 ; TITLE OF INVENTION: Anticoagulants
 ; FILE REFERENCE: 52295AUSM1
 ; CURRENT APPLICATION NUMBER: US/10/427,805
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/376,566
 ; PRIOR FILING DATE: 2002-05-01

NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456 fusion protein
 US-10-427-805-2
 Query Match 26.0%; Score 735; DB 12; Length 418;
 Best Local Similarity 50.5%; Pred. No. 3e-44;
 Matches 149; Conservative 18; Mismatches 55; Indels 73; Gaps 8;
 243 CAPRCQCPAGAAALQAD-GRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAAD 301
 150 GAPNFMLTQPHSVGASPGKTVTISCTRSSGVSASYVQVYQQRPGSSPTTV-----IYED 204
 302 QHRCEVDVDCILEPSPQPCOR---CVNT-----QGGFCHCYPNYDLV-- 340
 205 NHR-----PSGVDFRFGSITSSNSASLTISGLKTEDEADYVQSYDSNNLVVF 254
 341 -----DGECEVPEVDFCFRANCEYOCQPLNQTSLVCVCAEGF 376
 255 GGGTKLTVLGAAGGGGGGGGGVPEVDFCFRANCEYOCQPLNQTSLVCVCAEGF 314
 377 APIPHEPHRCQMFNCNQTACPADCDNTOASCCEPGYILDDGFICTDIDECENGFCSCGV 436
 315 APIPHEPHRCQMFNCNQTACPADCDNTOASCCEPGYILDDGFICTDIDECENGFCSCGV 374
 437 CHNLPGTFECICGPDALAHIGTDCDCKVDGSGSGEPPSPPTPGSTLTTPPA 491
 375 CHNLPGTFECICGPDALAHIGTDC-----AAAGAFVYVDFP---LEPRA 417

RESULT 12
 US-10-427-805-3
 ; Sequence 3, Application US/10427805
 ; Publication No. US20040063632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McLean, Kirk
 ; TITLE OF INVENTION: Anticoagulants
 ; FILE REFERENCE: 52295AUSM1
 ; CURRENT APPLICATION NUMBER: US/10/427,805
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/376,566
 ; PRIOR FILING DATE: 2002-05-01
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 397
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456delta fusio protein
 US-10-427-805-3
 Query Match 25.3%; Score 715; DB 12; Length 397;
 Best Local Similarity 55.0%; Pred. No. 7.5e-43;
 Matches 137; Conservative 14; Mismatches 38; Indels 60; Gaps 5;
 259 GRSCTASATQSCNDLCEHFCVFNPDQPGSYSCMCETGYRLAADQHRCEVDVDCILEPSPC 318
 164 GKTVTISCTRSSGVSASYVQVYQQRPGSSPTTV-----IYEDNHR-----PSGV 208
 319 POR---CVNT-----QGGFCHCYPNYDLV----- 340
 209 PDRFSGSIDTSSNSASLTISGLKTEDEADYVQSYDSNNLVWFGGKTLVLAAGAGGG 268
 341 -----DGECEVPEVDFCFRANCEYOCQPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNQT 393

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Db 269 SGGGSGGGSVPEVDFRFRANCEYQOPLNQTSLYLCVCAEGFAPIPHEPHRCQMFQNT 328
Qy 394 ACPADCDNTQASCECPGYILDDGFICTDIDECENGSGFCGVCNHLPGTPECICGPD 453
Db 329 ACPADCDNTQASCECPGYILDDGFICTDIDECENGSGFCGVCNHLPGTPECICGPD 388
Qy 454 LARHIGTDC 462
Db 389 LAGQIGTDC 397

RESULT 13
US-10-029-386-33151
; Sequence 33151, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33151
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL118508.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUATION 7.00e-44
US-10-029-386-33151

Query Match 20.6%; Score 582; DB 14; Length 645;
Best Local Similarity 31.8%; Pred. No. 3.7e-33;
Matches 176; Conservative 52; Mismatches 200; Indels 126; Gaps 31;

6 QPGGSQ-----CVEHDCFPALYPGATFLNASQICDGLRGLMTVRSVAAD----VI 53
17 QPGAGTGADTEAVVCGTACTYAHSGKLSAAEAQHNCNQNGLATVKSKEAQHVQVL 76
54 SLLNGDGGVGR--RLWIGLQLPPG-CGDKPLGLRGFOWVTGDNNTSYSRWARLDN 110
77 AQLRREALTARMKFWIGLQREKGLDPSL--PLKGFVWGGEDTFSNWHKELRN 134
111 GAPLCGPCLVA--VSAEAATVPSE-PIWEEQOC-----EVKADGFLCEHFPATCRPLA 161
135 SC--ISKRCVSLLDLSQLPLPSRLPKWSEGPCGSPGSGNIEGVCKFSFGKMCRLPLA 192
162 V-EPGAAAAVSYITPTFAARGADFOALPVGSSAAVAPLGLQLMC--TAPPGAVQGHM-- 217
193 LGPG-----QVTTTPTFTTSSSLEAVPFAAANVA-----CGEGDKDETQSHYFL 239
218 -AREAAGWD-----CSVENGGCEHAC-NAIPGAPRCQCPAGAAQADGRS 261
240 CKEAPDFVDMGSSGFLCVSPKYGCFNFGNGGCHQDCFEFGDGSFLGCRPGRLLDLVT 299
262 CTASATQSCNDLCE--HFCVPNPDPQSGYSYCMCTGTGRLAADQHRCEVDVDCILESPCP 319
300 C-ASRNPFCSSPCRGATCVLGP-HGKNYTCRCPOGYQLDSSQLDCVDVDEC--QDSPCA 355
320 QRCVNTQGGFECHCYPNYDLVDGECVPEVDFPFRANCEYQOPLNQTSLYLCVCAEGFAP 379
356 QECVNTPGFRCCEWVG-----EPGPG-----GEGACQDVDE-----CALGRSP- 395
380 PHEPHRCQMFQNTACPADCPNTQAS--CECPGYIL--DDGFICTDIDEC--ENGFC 433
396 -----CAQGC--TNTDGSFHCSEBEGVLAGEDTQCQDVDCVFGGFLC 439
434 SGVCHNLPGTPECICGPDLSALRHIGTDCSGKY-----DGGDSGSGE-----P 477

Db 269 SGGGSGGGSVPEVDFRFRANCEYQOPLNQTSLYLCVCAEGFAPIPHEPHRCQMFQNT 328
Qy 394 ACPADCDNTQASCECPGYILDDGFICTDIDECENGSGFCGVCNHLPGTPECICGPD 453
Db 329 ACPADCDNTQASCECPGYILDDGFICTDIDECENGSGFCGVCNHLPGTPECICGPD 388
Qy 454 LARHIGTDC 462
Db 389 LAGQIGTDC 397

RESULT 14
US-10-408-765A-1422
; Sequence 1422, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1422
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1422

Query Match 20.6%; Score 582; DB 16; Length 652;
Best Local Similarity 31.8%; Pred. No. 3.8e-33;
Matches 176; Conservative 52; Mismatches 200; Indels 126; Gaps 31;

6 QPGGSQ-----CVEHDCFPALYPGATFLNASQICDGLRGLMTVRSVAAD----VI 53
17 QPGAGTGADTEAVVCGTACTYAHSGKLSAAEAQHNCNQNGLATVKSKEAQHVQVL 76
54 SLLNGDGGVGR--RLWIGLQLPPG-CGDKPLGLRGFOWVTGDNNTSYSRWARLDN 110
77 AQLRREALTARMKFWIGLQREKGLDPSL--PLKGFVWGGEDTFSNWHKELRN 134
111 GAPLCGPCLVA--VSAEAATVPSE-PIWEEQOC-----EVKADGFLCEHFPATCRPLA 161
135 SC--ISKRCVSLLDLSQLPLPSRLPKWSEGPCGSPGSGNIEGVCKFSFGKMCRLPLA 192
162 V-EPGAAAAVSYITPTFAARGADFOALPVGSSAAVAPLGLQLMC--TAPPGAVQGHM-- 217
193 LGPG-----QVTTTPTFTTSSSLEAVPFAAANVA-----CGEGDKDETQSHYFL 239
218 -AREAAGWD-----CSVENGGCEHAC-NAIPGAPRCQCPAGAAQADGRS 261
240 CKEAPDFVDMGSSGFLCVSPKYGCFNFGNGGCHQDCFEFGDGSFLGCRPGRLLDLVT 299
262 CTASATQSCNDLCE--HFCVPNPDPQSGYSYCMCTGTGRLAADQHRCEVDVDCILESPCP 319
300 C-ASRNPFCSSPCRGATCVLGP-HGKNYTCRCPOGYQLDSSQLDCVDVDEC--QDSPCA 355
320 QRCVNTQGGFECHCYPNYDLVDGECVPEVDFPFRANCEYQOPLNQTSLYLCVCAEGFAP 379
356 QECVNTPGFRCCEWVG-----EPGPG-----GEGACQDVDE-----CALGRSP- 395
380 PHEPHRCQMFQNTACPADCPNTQAS--CECPGYIL--DDGFICTDIDEC--ENGFC 433
396 -----CAQGC--TNTDGSFHCSEBEGVLAGEDTQCQDVDCVFGGFLC 439
434 SGVCHNLPGTPECICGPDLSALRHIGTDCSGKY-----DGGDSGSGE-----P 477

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Wed Jun 9 13:16:02 2004

Job time : 44 secs

Db 440 DSLCFNTQSFHCGCLPGWVLAPN-GVSCMTGMPVSLGPPSGPDEEDKGEKSGSTVPRAA 498

Qy 478 PPSPTPGSTLTTPA 491

Db 499 TASPTRGEGTTPKA 512

RESULT 15

US-09-789-919-96
; Sequence 96. Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; APPLICANT: Moore, Kateri
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789,919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-789-919-96

Query Match 20.5%; Score 580; DB 9; Length 652;
Best Local Similarity 31.6%; Pred. No. 5.2e-33;
Matches 175; Conservative 53; Mismatches 200; Indels 126; Gaps 31;

Qy 6 QPGGSG-----CUEHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAAD---VI 53
Db 17 QPGAGTCADTEAVVVCVTACTYTAHSGKLSAAEAQNHCNONGNLTATVKSKEAAQHVQVRL 76
Qy 54 SILLNGDGVGR--RLWIGLQLPPG-CGDPKRLGLRGLFQWVTGDNNTSYSRWRLDLN 110
Db 77 AQLRREALTARMSFWIGLQREKGLCLDPSL--PLKGFVWVGGEDTPYSNWHKELRN 134
Qy 111 GAPLCGLCVA--VSAEAETVPS--PIWEQOC-----EVKADGFLCEHFFPATCRPLA 161
Db 135 SC--ISKRCVSLLLDLSQLPNRLPKWSEGPCSGSPGSNIEGFVKFSPKGMCRPLA 192
Qy 162 V-EFPAAGAAVSTYGTTPFAARGADFOALFVGSSAAVAPLGLQIMC-TAPPGAVQGHW-- 217
Db 193 LGGFG-----QVYTTTPTTSSLEAVFPAAANVA-----CGEGKDETQSHYFL 239
Qy 218 -AREAPGAWD-----CSVENGGCEHAC-NAIPGAPRCQCPAGALQADGRS 261
Db 240 CKEKAPVDFWNGSSGPLCVSPKYGCFNNGGCHQDCPEGGDGSFLCGCRPGRLLDLVT 299
Qy 262 CTASATOSCNDLCE--HFCVNPDPQGSYSYCMCTGYRLAADQHRCEVDVDDCILEPSPCP 319
Db 300 C-ASRNPCSSSPCRGGATCVLGP-HGKNYTCRCPCQGYQLDSSQLDCVDVDEC--QDSPCA 355
Qy 320 QRCVNTQGGECYCNVYDLVDGCVBPVDFCFRANCEYOCQPLNQTXYLCVCAEGFAP 379
Db 356 QECVNTPGGFRCRCWVG-----EPGGP-----GEGACQVDDE-----CALGRSP- 395
Qy 380 PHEPHRCQMFNCQACPADCDPNTQAS--CRCPGEGYIL--DDGFICTDIDEC--ENGGFC 433
Db 396 -----CAQGC-TNTDGSFHCSEEGYVLAGEDGTQCQDVDECVGFGGGLC 439
Qy 434 SGVCHNLPFTFECIGPDSALARIHIGTDCDSKV-----DGDGSGGE-----P 477
Db 440 DSLCFNTQSFHCGCLPGWVLAPN-GVSCMTGMPVSLGPPSGPDEEDKGEKSGSTVPRAA 498
Qy 478 PPSPTPGSTLTTPA 491
Db 499 TASPTRGEGTTPKA 512

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:44:08 ; Search time 16.5 Seconds
(without alignments)
2903.235 Million cell updates/sec

Title: US-09-509-994-2_COPY_19_516
Perfect score: 2830
Sequence: 1 APABPQGGSCQVHDFAL.....PSPTFGSLTPPAGLVHSG 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2826	99.9	575	1 THHUB	thrombomodulin pre
2	1858	65.7	577	2 A60501	thrombomodulin pre
3	1095.5	38.7	356	2 A25918	thrombomodulin - b
4	414	14.6	1574	2 T13954	MEGF6 protein - ra
5	414	14.6	1620	2 T27283	hypothetical prote
6	374	13.2	2907	2 A57278	fibrillin-2 precu
7	368	13.0	2871	2 A55567	fibrillin 1 - bovi
8	367.5	13.0	1184	2 A55184	fibulin-2 precurs
9	366	12.9	2918	2 A54105	fibulin-2 precu
10	364	12.9	3002	2 A47221	fibrillin 1 precu
11	362	12.8	2871	2 A55624	fibrillin-1 precu
12	357	12.6	741	2 T46488	hypothetical prote
13	357	12.6	1221	2 A49457	fibulin-2 precurs
14	332.5	11.7	1964	2 T09059	notch4 - mouse
15	331	11.7	589	2 T43210	fibulin-1D precurs
16	330.5	11.7	1712	2 A38261	masking protein pr
17	324.5	11.5	689	2 T42760	fibulin, splice fo
18	324.5	11.5	712	2 T42990	fibulin 1, splice
19	322.5	11.4	1394	2 A35626	transforming growt
20	321	11.3	2321	2 T78549	notch3 protein - h
21	314.5	11.1	3507	2 T34513	hypothetical prote
22	313	11.1	798	2 T22793	hypothetical prote
23	312.5	11.0	1820	2 A55494	latent transformin
24	311	11.0	601	2 B36346	fibulin 1 precurs
25	311	11.0	683	2 C36346	fibulin 1 precurs
26	309	10.9	685	2 S78040	fibulin, splice fo
27	308	10.9	705	2 S34968	fibulin, splice fo
28	303.5	10.7	1251	2 A57293	latent transformin
29	297	10.5	2531	2 A46019	notch-1 protein -

30	287	10.1	2471	2 A49128	cell-fate determin
31	285	10.1	2352	2 T30201	Notch homolog prot
32	284.5	10.1	2437	2 S42612	transmembrane prot
33	280.5	9.9	2703	1 A24420	notch protein - fr
34	280	9.9	2318	2 S45306	notch 3 protein -
35	279.5	9.9	387	2 T138449	extracellular prote
36	277.5	9.8	511	2 T17298	hypothetical prote
37	276.5	9.8	493	2 JC5621	epidermal growth f
38	276	9.8	2531	2 S18188	notch protein homo
39	273	9.6	2555	2 A40043	epidermal growth f
40	269.5	9.5	1217	1 E0MSMG	Notch B protein -
41	264	9.3	1203	2 A49175	notch homolog - se
42	263.5	9.3	2531	2 T31070	Notch protein - Af
43	256.5	9.1	2524	2 A35844	growth potentiatio
44	254.5	9.0	674	2 T55476	growth arrest-spec
45	249	8.8	678	2 B48089	

ALIGNMENTS

RESULT 1

THHUB
thrombomodulin precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence revision 12-May-1995 #text change 15-Sep-2000
C:Accession: A41442; A28307; A29680; A27073; JX0264; S38954
R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama J. Biochem. 103, 281-285, 1988
A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activ
A:Reference number: A41442; MUID:88227901; PMID:2836377
A:Accession: A41442
A:Molecule type: DNA
A:Residues: 1-575 <SHL>
A:Cross-references: DBJ:D00210; NID:G220126; PIDN:BAA00149.1; PID:G220127
R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
A:Reference number: A28307; MUID:87317665; PMID:2819876
A:Accession: A28307
A:Molecule type: DNA; mRNA
A:Residues: 1-472, 'A', 474-575 <JAC>
A:Cross-references: GB:J02973; NID:G339658; PIDN:AAA61175.1; PID:G339659
R:Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioaka, J.; Maruyama, I.; Zushi, M.; Kawaha
EMBO J. 6, 1891-1897, 1987
A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
A:Reference number: A29680; MUID:88004395; PMID:2820710
A:Accession: A29680
A:Molecule type: mRNA
A:Residues: 1-575 <SUZ>
A:Cross-references: GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G736251
A:Experimental source: lung endothelium
A:Note: part of this sequence, including the amino end of the mature protein, were deter
R:Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
Biochemistry 26, 4350-4357, 1987
A:Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
A:Reference number: A27073; MUID:88024950; PMID:2822087
A:Accession: A27073
A:Molecule type: mRNA
A:Residues: 1-472, 'A', 474-575 <WEN>
A:Cross-references: GB:M16552; NID:G339656; PIDN:AAB59508.1; PID:G339657
A:Experimental source: placenta
A:Note: parts of this sequence were determined by protein sequencing
R:Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
J. Biochem. 113, 433-440, 1993
A:Title: Urinary thrombomodulin, its isolation and characterization.
A:Reference number: JX0264; MUID:93293792; PMID:8390446
A:Accession: JX0264
A:Molecule type: protein; mRNA
A:Residues: 19-472, 'A', 474-486 <YAM>
A:Experimental source: urine
A:Note: the urinary form appears to be identical with that circulating in plasma
R:Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grimell, B.W.

Biochem. J. 295, 131-140, 1993
 A;Title: Identification of the predominant glycosaminoglycan-attachment site in soluble serine.
 A;Reference number: S38954; MUID:94029900; PMID:8216207
 A;Accession: S38954
 A;Molecule type: protein
 A;Residues: 475-491, X, 493-494 <GER>
 A;Note: the residue designated 'X' was determined to be a Ser with covalently bound chondroitin sulfate.
 R;Meininger, D.P.; Komives, E.A.
 submitted to the Brookhaven Protein Data Bank, September 1995
 A;Reference number: A67369; PDB:1ZAO
 A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues 475-491
 R;Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, August 1994
 A;Reference number: A52804; PDB:1HLT
 A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 submitted to the Brookhaven Protein Data Bank, November 1995
 A;Reference number: A65583; PDB:1FGD
 A;Contents: annotation; conformation by (1)H-NMR, residues 427-444
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 Protein Sci. 5, 195-203, 1996
 A;Title: Structural resiliency of an EGF-like subdomain bound to its target protein, thrombospondin-1.
 A;Reference number: A58595; MUID:96276211; PMID:8745396
 A;Contents: annotation; conformation by (1)H-NMR
 C;Genetics:
 A;Gene: GDB:THBD
 A;Cross-references: GDB:119613; OMIM:188040
 A;Map position: 20p11.2-20p11.2
 A;Introns: #status absent
 C;Complex: homodimer, urinary form
 C;Function:
 A;Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activation of plasminogen.
 A;Pathway: blood coagulation/moderation
 A;Note: the membrane-bound form is located on the endothelium luminal surface of arteries and is subject to endocytosis.
 C;Superfamily: thrombospondin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; protein
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-575/Product: thrombospondin, membrane-bound form #status predicted <MAT>
 F;19-513/Domain: extracellular #status predicted <EXT>
 F;19-486/Product: thrombospondin, urinary form #status experimental <MAU>
 F;24-167/Domain: C-type lectin homology <LCH>
 F;177-199/Region: PEST sequence
 F;201-233/Region: PEST sequence
 F;245-280/Domain: EGF homology <EG1>
 F;288-323/Domain: EGF homology <EG2>
 F;329-362/Domain: EGF homology <EG3>
 F;369-404/Domain: EGF homology <EG4>
 F;408-439/Domain: EGF homology <EG5>
 F;445-480/Domain: EGF homology <EG6>
 F;485-513/Region: PEST sequence
 F;517-539/Domain: intracellular #status predicted <TMN>
 F;540-575/Domain: transmembrane #status predicted <INT>
 F;47, 115, 116, 382, 409/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;174, 225, 411, 504/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F;245, 256, 252, 265, 267, 280, 288, 292, 308, 310, 323, 329, 340, 336, 349, 351, 362, 369, 378, 374-38
 F;334, 498/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F;490, 492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimental

Query Match 99.9%; Score 2826; DB 1; Length 575;
 Best Local Similarity 99.8%; Pred. No. 2e-162;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 APAPPPQGGSCVHDCFPALPGPATFNLASQICDGLRGLHMTVRSSVAADVLSILLNGD 60
 19 APAPPPQGGSCVHDCFPALPGPATFNLASQICDGLRGLHMTVRSSVAADVLSILLNGD 78
 61 GGVGRRRLWIGLQPLPPGCGDKPKRLGFLRGFQWVTGDNNTSYSRWALDLNGLPCLCV 120
 79 GGVGRRRLWIGLQPLPPGCGDKPKRLGFLRGFQWVTGDNNTSYSRWALDLNGLPCLCV 138

QY 121 AVSAAEATVPSEPIWEQQCEVKADGFLCEHFFPATCRPLAVEPAAAAAASITTYTTPA 180
 DB 139 AVSAAEATVPSEPIWEQQCEVKADGFLCEHFFPATCRPLAVEPAAAAAASITTYTTPA 198
 QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGAVQGHWAREAPGAWDCSVENGCCCHACNA 240
 DB 199 ARGADFOALPVGSSAAVAPLGLQLMCTAPPAGAVQGHWAREAPGAWDCSVENGCCCHACNA 258
 QY 241 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
 DB 259 IFGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 318
 QY 301 DQHRCEVDVDDCILEPSPQRCVNTQSGFECHYCNLYDLDGECVPEVDPCEFRANCEYQC 360
 DB 319 DQHRCEVDVDDCILEPSPQRCVNTQSGFECHYCNLYDLDGECVPEVDPCEFRANCEYQC 378
 QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNCTACPDNPTQASCECEGYILLDDGFI 420
 DB 379 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNCTACPDNPTQASCECEGYILLDDGFI 438
 QY 421 CTIDECENGGFCGVCNHLPGTFECICGPDSSALAHHTGDCDCKVGDGSGSGEPPEPS 480
 DB 439 CTIDECENGGFCGVCNHLPGTFECICGPDSSALAHHTGDCDCKVGDGSGSGEPPEPS 498
 QY 481 PTFGSTLTTPPAVGLVHSG 498
 DB 499 PTFGSTLTTPPAVGLVHSG 516

RESULT 2
 A60501
 thrombospondin precursor - mouse
 N;Alternate names: fetomodulin
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 16-Jul-1999
 A;Accession: S08488; A32001; A60501
 R;Dittman, W.A.; Majerus, P.W.
 Nucleic Acids Res. 17, 802, 1989
 A;Title: Sequence of a cDNA for mouse thrombospondin and comparison of the predicted mouse
 A;Reference number: S08488; MUID:89128454; PMID:2536925
 A;Accession: S08488
 A;Molecule type: mRNA
 A;Residues: 1-577 <DIT>
 A;Cross-references: EMBL:X14432; NID:g54781; PIDN:CAA32597.1; PID:g54782
 R;Dittman, W.A.; Kumada, T.; Sadler, J.E.; Majerus, P.W.
 J. Biol. Chem. 263, 15815-15822, 1988
 A;Title: The structure and function of mouse thrombospondin. Phorbol myristate acetate st
 A;Reference number: A32001; MUID:89008498; PMID:2844823
 A;Accession: A32001
 A;Molecule type: mRNA
 A;Residues: 97-577 <DI2>
 A;Cross-references: GB:J04060
 R;Imada, S.; Yamaguchi, H.; Nagumo, M.; Katayanagi, S.; Iwaseki, H.; Imada, M.
 Dev. Biol. 140, 113-122, 1990
 A;Title: Identification of fetomodulin, a surface marker protein of fetal development, as
 A;Reference number: A60501; MUID:90292331; PMID:2162790
 A;Accession: A60501
 A;Molecule type: protein
 A;Residues: 19-22;330-343;479-489;545-555;562-575 <IMA>
 C;Comment: Thrombospondin binds to and internalizes with thrombin. It is also a cofactor
 C;Superfamily: thrombospondin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; membrane protein; phosphoprotein; receptor
 F;24-165/Domain: C-type lectin homology <LCH>
 F;244-279/Domain: EGF homology <EG1>
 F;287-322/Domain: EGF homology <EG2>
 F;328-361/Domain: EGF homology <EG3>
 F;368-403/Domain: EGF homology <EG4>
 F;407-438/Domain: EGF homology <EG5>
 F;444-479/Domain: EGF homology <EG6>

Query Match 65.7%; Score 1858; DB 2; Length 577;
 Best Local Similarity 66.0%; Pred. No. 2.2e-104;

	Matches	332;	Conservative	45;	Mismatches	118;	Indels	8;	Gaps	4;								
Qy	1	APAE	PQGSQCV	EHDC	FALYPGPAT	FLNASQICDGLR	GLHMTV	RSSVAAD	VISILLNG	60								
Db	19	ALAKI	QPTGSQCV	EHCFAL	FGP	PATFLDASQACQ	RLQGHMTV	RSSVAAD	VISILLSS	78								
Qy	61	G-GVGR	RLWIGLQI	PPGCGD	PKRIGPLRG	FWQWTTGD	NNTSYSR	WARLDING	APLCGPLC	119								
Db	79	SMDLGP	--WIGLQI	PQGCDD	PVHLGR	PLRGFWVT	GDNHTSYS	RWARPN	DOTAPLCGPLC	135								
Qy	120	VAVSAEA	ATVPSEPI	TEWEEO	QCEKADG	FLCEHF	FPATCR	PLAVEP	-GAAAAA	VSIITYGP	178							
Db	136	VTVSTATEA	APGEP	AWEKPECT	ETGFCF	EYFTASCR	PLTWNTD	DPRAH	ISSIYNTP	195								
Qy	179	FAARGAD	FQALPVG	SAAVAP	LGLQLMCT	APPAQVQ	QHWAREA	PGAWD	CSVNGG	CEHAC	238							
Db	196	FGVSGAD	FQTLPVG	SAAVEPL	GLELVC	RAPPGT	SEGHWA	WEATGAWN	CSVNGG	CEYLC	255							
Qy	239	NAIPGA	PRCCPQ	CAGAA	LQADGR	SCTASAT	QSCNDL	CEHF	CVNPD	OPGVS	CMCTGYRL	298						
Db	256	NRSTNE	PRCLCP	RDMDL	QADGR	SCARPV	QSCNEL	CEHF	CVSNAE	VEPGS	CMCTGYQL	315						
Qy	299	AADQHR	CEDVDD	CILBPS	PCPCRV	ANTQGF	CECHCY	PNYDL	VNDC	ECVEP	VDPCFRANCEY	358						
Db	316	AADGHR	CEDVDD	CKQGNP	CFQCVN	TKGFE	CFCYDGY	BLVD	GVGCE	VELLD	PCFGSMCEP	375						
Qy	359	QCQPL	NQTSVLC	VAEG	FAPIPHE	PHRCM	FCNQTAC	PACD	CDPNT	QASCE	CPGYYILDDG	418						
Db	376	QCQPV	SPDTR	YRCICAP	GA	EPADPE	PHKEM	FCNET	SCPAD	CDPNS	PVCECP	SGFILDEG	435					
Qy	419	FICTD	IDECE	NGGFC	SGVCHN	LPGTF	ETFCICG	PD	SALAR	HI	GTDCD	SGKV---	475					
Db	436	SVCTD	IDE	CSQ	CECFT	SECRN	FP	SGSY	ECICG	PD	TALAG	QISK	CDP	PV	AREDT	KEE	EGSG	495
Qy	476	EP	PPSP	PTG	STLTP	PAVGL	VHSG	498										
Db	496	EP	VS	PTG	SP	TP	PP	SP	AR	PV	HS	518						

RESULT 3
A25918
thrombomodulin - bovine (fragment)
C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C.Accession: A25918
R.Jackman, R.W.; Beesler, D.L.; VanDeWater, L.; Rosenberg, R.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 8834-8838, 1986
A.Title: Characterization of a thrombomodulin cDNA reveals structural similarity to the
A.Reference number: A25918; MUID:97067408; PMID:3024152

A:Accession: A25918
 A:Molecule type: mRNA
 A:Residues: 1-356 <UAC>
 A:Cross-references: GB:M14657; NID:g163762; PID:AA30785.1; PID:g163763
 C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: transmembrane protein
 C:Keywords: <EGL>
 F:21-56/Domain: EGF homology <EG1>
 F:64-97/Domain: EGF homology <EG2>
 F:103-136/Domain: EGF homology <EG3>
 F:143-178/Domain: EGF homology <EG4>
 F:182-213/Domain: EGF homology <EG5>
 F:219-253/Domain: EGF homology <EG6>

[illegible]

331 CHCVPNYDLVDEGCEVDPDCEFRANCEYCCOCPNLTSLVCACGFAFAPLPHBPHRCOMFC 390
123 CHDGTGYELVDEGCEVDPDPCFDNCCETQCPQVGRSEHKICIAEGFAFVPGGAPHKCOMFC 182
391 NOTACPADCDNTQASCSPGYILDDGFICTDIDCECENGFCGVCNHLPGTFCICGP 450
183 NQTSFADCDPHYPTICRCPGYIIDEGSTPDINECDT-NTCPQCHNLPGTFCICGP 241
451 DSALARHGTDCDSKV-----DGGDSGSGEPPPTPGSTLTP-PA-VGLVHSG 498
242 DSALSGOIGIDCDPTGVNNEGTPTSDYG--GSGEPVPTPGATARSPAPAGPLHSG 297

RESULT 4

Tl3954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: Tl3954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MCID:98360089; PMID:9693030
A:Accession: Tl3954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 14.6%; Score 414; DB 2; Length 1574;
Best Local Similarity 34.1%; Pred. No. 1.8e-17;
Matches 104; Conservative 28; Mismatches 101; Indels 72; Gaps 17;

[illegible]

RESULT 5

T27283
 C:Accession: T27283
 R:Ainscough, R.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20336
 A:Accession: T27283
 A:Status: preliminary; translated from SE/EMBL/DDBJ

1288 DGQCTNIFGVRCLCYDGFMSMDMKTCDVNECDLNPNCMFCECENTKGSFICHQCL 1347
 336 NYDLVDGE--CVEPVDPC--FRANCYQCOPLN-QTSYLCVCAEGFA-----PIP 380
 1348 GYSVKGGTGTCTD-VDECEIGHNCDMHASCLNVPVGSFKSCREGWVGNGIKCIDLDECA 1406
 381 HEPHRCOMFCNQTACADCPNTOAS--CECPGYILDDGFICTDIDE-----CENG- 430
 1407 NGTHQCSI-----NAQC-VNTPGSYRCACSEGF-TGDTGFTSDVDECAENLNCENGQ 1457
 431 -----GF-----CS-----GVCHNLPGTFFCICGPDGALA 455
 1458 CLNVPVGAIRCECEMGFTFASDRSQRCDIDECSEFONICVFGTCNNLPGMFHICIDGVELD 1517
 456 RHIG--TDGD 463
 1518 RTGNCCTDID 1527

RESULT 7
 A55567
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Nov-2003
 C:Accession: A55567
 R:Illustra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
 Genomics 23, 480-485, 1994
 A:Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to
 A:Reference number: A55567; MUID:95137597; PMID:7835900
 A:Accession: A55567
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2871 <full>
 A:Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428
 C:Superfamily: fibrillin; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 13.0%; Score 368; DB 2; Length 2871;
 Best Local Similarity 31.5%; Pred. No. 1.6e-14;
 Matches 111; Conservative 26; Mismatches 109; Indels 106; Gaps 20;

226 DCSVNGGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPV--- 282
 1200 ECSIMNGGCTCTNSEGSEYCSQCPGFALPDQASCT-----DIDE--CEDNPNIC 1249
 283 -----DQGSYSYCMCTGYRLAADOHRCEVDVDCILEPSPC-PQRCVNTQGFCHCYP 335
 1250 DGQCTNIFGVRCLCYDGFMSMDMKTCDVNECDLNPNCMFCECENTKGSFICHQCL 1309
 336 NYDLVDGE--CVEPVDPC--FRANCYQCOPLN-QTSYLCVCAEGFA-----PIP 380
 1310 GYSVKGGTGTCTD-VDECEIGHNCDMHASCLNVPVGSFKSCREGWVGNGIKCIDLDECS 1368
 381 HEPHRCOMFCNQTACADCPNTOAS--CECPGYILDDGFICTDIDE-EN----- 429
 1369 NGTHMCSQH-----ADC-KNTMGSYRCLCKEY-TGDTGFTCTDLDSENLNLCNGQ 1419
 430 -----GGF-----CS-----GVCHNLPGTFFCICGPDGALA 455
 1420 CLNAPGVYRCCEMDGVFVSADGKACEDIDECSEFONICVFGTCNNLPGMFHICIDGVELD 1479
 456 RHIG--TDGD 463
 1480 RSGNCTDYNCELDPTTCISGNCVNTPGSYTCDPCPD-----FELNPRVGCV 1527

RESULT 8
 A55184
 fibulin-2 precursor - human
 N:Alternate names: protein DKFZp586A1519.1
 C:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 08-Sep-2002

A:Molecule type: DNA
 A:Residues: 1-1620 <full>
 A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
 A:Experimental source: clone Y64G10A
 C:Genetics:
 A:Gene: CESP:Y64G10A.f
 A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 14.6%; Score 414; DB 2; Length 1620;
 Best Local Similarity 27.0%; Pred. No. 1.8e-17;
 Matches 128; Conservative 38; Mismatches 176; Indels 132; Gaps 20;

101 YSRWARLDNAPLCGPICVASAAE-----ATVPSEPIWEBOQCE--VKADGFICEF 151
 56 YLRPAPFRRGCKCLLRQVANCADLCHNGGTCPSEHNDNEQVCEPCVGTGAKCOY 115
 152 HFPATCRPLAVEPGAAAVSITYGTPFAARGADFOALPVSSAAVPLGLQMLCTAPP 211
 116 D-ANEC--MANNGGCEHCVN-TIGTY-----CRWPG 145
 212 AVQGHWAREAPGAWDCSVENGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSC- 270
 146 FELSDGNTCSIDISCAVNGGCSRCVNSPGFRCDCPSDLYLHADGRTC--GKVTSCS 203
 271 --NDLCEHFCVNPVPPQGSYSYCMCTGYRLAADOHRCEVDVDCILEPSPCPORCVNTQGG 328
 204 TDNGGCEHEC-ENDSNGEYRCRCRVGFSLSENKSCQVDPDFNKGCGQHCTNNHGR 262
 329 FECHYVNTDL-VDBECVFPVPCFRAN-CEYQCOPLNQTSLYLCVCAEGFAPIPEPHRC 386
 263 AOCQCYEGFHLSDYRRSCVDIDECADKNGCEHFCENVKGT-YRCKREGY-QIQRDGRTC 320
 387 OMF-----CNQATACPADC--DNPQASCECPGYYL----- 415
 321 EEMLGCGVNGGCGQHDQVDPDGGHVKCRNGYILLANDKQLCHDNISVTHARAPRLWD 380
 416 -----DDGF-----ICTDIDE-ENGFCGSGVC 437
 381 SYETVTCVTPTDLTCHKLMHLDGSHVQCFDDGYELIDSKFCQDINECHENNGDCSQIC 440
 438 HNLPGTFFCICGPDGALAHIGT-----DCDS-----GKVDGDSGSGEP 477
 441 VNLAGSVEQCKPGLMKDRKTCEDISECSSNNGGCEYCSNQEGYWCSCPE 494

RESULT 6
 A57278
 fibillin-2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 24-Nov-2003
 C:Accession: A57278
 R:Zhang, H.; Hu, W.; Ramirez, F.
 J. Cell Biol. 129, 1165-1176, 1995
 A:Title: Developmental expression of fibillin genes suggests heterogeneity of extracell
 A:Reference number: A57278; MUID:95263670; PMID:7744963
 A:Accession: A57278
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2907 <ZHA>
 A:Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
 C:Superfamily: fibrillin; EGF homology
 F:1239-1274/Domain: EGF homology <EGF1>
 F:2488-2523/Domain: EGF homology <EGF>

Query Match 13.2%; Score 374; DB 2; Length 2907;
 Best Local Similarity 32.9%; Pred. No. 7.2e-15;
 Matches 102; Conservative 24; Mismatches 92; Indels 92; Gaps 18;

226 DCSVNGGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPV--- 283
 1238 EGMVNGGCTDQCTNSEGSEYCSQCPGFALPDQASCT-----DIDE--CEDNPNIC 1287
 284 -----DQGSYSYCMCTGYRLAADOHRCEVDVDCILEPSPC-PQRCVNTQGFCHCYP 335

RESULT 8
 A55184
 fibulin-2 precursor - human
 N:Alternate names: protein DKFZp586A1519.1
 C:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 08-Sep-2002

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2918 <ZHA>
A;Cross-references: GB:703272
R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17063

A;Molecule type: mRNA
A;Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>
A;Cross-references: EMBL:X62009
R;Milewicz, D.M.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31101
A;Accession: S31101

A;Molecule type: mRNA
A;Residues: 752-1407, 'R', 1409-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 192
A;Cross-references: EMBL:X62009
C;Genetics:
A;Gene: GDB:FBN2
A;Cross-references: GDB:128122; OMIM:121050
A;Map position: 5q23-5q31
A;Superfamily: fibrillin; EGF homology
C;Keywords: extracellular protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-2918/Product: fibrillin-2 #status predicted <MAT>
F;1245-1280/Domain: EGF homology <EGF1>
F;1970-2013/Domain: EGF homology <EGF>

Query Match 12.9%; Score 366; DB 2; Length 2918;
Best Local Similarity 33.1%; Pred. No. 2.2e-14;
Matches 101; Conservative 25; Mismatches 97; Indels 82; Gaps 17;
Qy 226 DCSVNGGCHACNAIPGAPRCQCPAGALQADGRSCTASATOSCNLDCEHFCVNPDP-- 283
Db 1244 ECMIMNGGDTCTNSGSEYSCSEGVAMPDGRSCA-----DIDE--CENNEDIC 1293
Qy 284 -----QPGSYCMCTGYRLAADQHRCEVDVDCILEPSPCP-QRCVNTGGFECCHCP 335
Db 1294 DGGQCTNIPGYRCLCYDGFMSMDKTCIDVNECDLNSNCFMGECENTKGSFICHL 1353
Qy 336 NYDLVDBE--CUEPVDPC--FRANCEVCCQLN-QTSYLCVCAGFAPIPH-----EPHR 385
Db 1354 GYSVKKGTGTCTD-VDECEIGHNCDHMASCLNIPGSKCSREGW--IGNGIKCIDLDE 1410
Qy 386 COMFCNQACPADCDPNTQAS--CECPGYILDGFICTDIDE-----CENG----- 430
Db 1411 CNGTHQCSINAQC-VNTPGSVRCACSEGF-TGDGFTGSDVDECAENLNCENGQCLNVP 1468
Qy 431 -----GF-----CSGVCHNLPGTPECICGPDALARHIG- 459
Db 1469 GAYRCECEMGFTPASDRSCQDIBCSFQNICVSGTCNNLPQMFHCICDDGYELDRGTGN 1528
Qy 460 -TDGD 463
Db 1529 CTDID 1533

RESULT 10
A47221
fibrillin 1 precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence revision 25-Apr-1997 #text change 24-Nov-2003
C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198
R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993
A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structu
A;Reference number: A47221; MUID:94010947; PMID:7691719
A;Accession: A47221
A;Molecule type: mRNA
A;Residues: 1-337, 'T', 339-1029 <COR>
A;Cross-references: GB:X63556

C;Accession: A55184; T08744
R;Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.
Genomics 22, 425-430, 1994
A;Title: Fibrillin-2 (FBN2): human cDNA sequence, mRNA expression, and mapping of the gen
A;Reference number: A55184; MUID:95104855; PMID:7806230
A;Accession: A55184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1184 <ZHA>
A;Cross-references: GB:X82494; NID:9575232; PIDN:CAA57876.1; PID:9575233
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08744

A;Molecule type: mRNA
A;Residues: 656-719, 'QDELMGHDCRRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCV', 720-853, 'T', 855-11
A;Cross-references: EMBL:AL050095
A;Experimental source: adult uterus; clone DKFZp586A1519
C;Genetics:
A;Gene: GDB:FBN2
A;Cross-references: GDB:293037; OMIM:135821
A;Map position: 3p25-3p24
A;Note: DKFZp586A1519.1
C;Superfamily: fibrillin-2; EGF homology; von Willebrand factor type C repeat homology
C;Keywords: alternative splicing; extracellular matrix
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-1184/Product: fibrillin-2 protein #status predicted <MAT>
F;905-941/Domain: EGF homology <EGF>

Query Match 13.0%; Score 367.5; DB 2; Length 1184;
Best Local Similarity 30.0%; Pred. No. 8.6e-15;
Matches 119; Conservative 29; Mismatches 124; Indels 125; Gaps 21;
Qy 136 BEQCEVKAD-GFCEHFFATC-----RPLAV-----BFGAAAAVSIYTPFAARG 183
Db 531 EGQCESNPNIYGPNC-HVMSCEGEPLIVPEVRPPPEAAPRRVS-----EAEM 582
Qy 184 ADFQALPVGSAAV---APLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCGEACNA 240
Db 593 AGREALSLGTAEALNSLPGLDQDELLPGBEL-----COHLGIN 622
Qy 241 IPGAPRCQCPAGALQADGRSC-----TASAT-----QS 269
Db 623 TVGSHYKACFPGLSLQDDGTCRPEGHPQPEAPPEALKSFQVANSNTPPLPQNT 682
Qy 270 QND--LCEHFCVNPDPQSGYSCMCTGYRLAADQHRCEVDVDCILEPSPCP--QRCVNT 325
Db 683 CKDNGPKQVC---STVGGSAICSEFPGYAIDAGVSCEDINECVTDLHTCSRGEHCNT 739
Qy 326 QGGFECH---CVPNYDLVDGCEVPEVDFFRANCEYQCPQLNQTSLCV----- 371
Db 740 LGSFHYKALTCEFGYALKDGE-EDVDEC--AMGHTTCQP---GFLCNTKGSFYCOA 792
Qy 372 ---CAEGFAPIPH-----EPHRCMFQNTACPADCDPNTQASCECPGY-I 414
Db 793 RQRCDMGFLQDPGNCVDINECTSLSEPCKPFGSCINTVGSYTCQRNPLI---CARGIHA 849
Qy 415 LDGFICTDDECEGFCGSG---VCHNLPGTPECIC 448
Db 850 SDPGAKCVDNCEGTGVRHCGEGVCHNLPGSYRCD 886

RESULT 9
A54105
fibrillin-2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text change 24-Nov-2003
C;Accession: A54105; S17063; S31101
R;Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguinetti, C.; Bonadio, J.; Mecham,
J. Cell Biol. 124, 855-863, 1994
A;Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefe
A;Reference number: A54105; MUID:94165150; PMID:8120105
A;Accession: A54105

R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Panglilan, T.; Bonadum. Mol. Genet. 2, 961-968, 1993
A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene in Marfan syndrome.
A;Reference number: 154355; MUID:93372860; PMID:8364578
A;Accession: 154355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 132-3002 <PER>
A;Cross-references: GB:113923; NID:g306745; PIDN:AAB02036.1; PID:g306746
R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
Nature 352, 334-337, 1991
A;Title: Partial sequence of a candidate gene for the Marfan syndrome.
A;Reference number: S17064; MUID:91304568; PMID:1852207
A;Accession: S17064
A;Molecule type: mRNA
A;Residues: 1030-3002 <MAS>
A;Cross-references: EMBL:X63556
R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A;Reference number: 159574; MUID:93157831; PMID:8430317
A;Accession: 159574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 2217-2288, '1', 2290-2325 <RES>
A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861
R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattel, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different chromosomes.
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17062
A;Molecule type: mRNA
A;Residues: 'VLTVVFILSYNKM', 944-1444 <LEE1>
A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015
A;Accession: S62111
A;Molecule type: protein
A;Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>
R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A;Title: Connective tissue microfibrils. Isolation and characterization of three large polypeptides.
A;Reference number: A34198; MUID:90078246; PMID:2512293
A;Accession: A34198
A;Molecule type: protein
A;Residues: 565-575; 1890-1892, 'I', 1894-1900 <MAD>
C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
C;Genetics:
A;Gene: GDB:FBN1
A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
A;Map position: 15q21.1-15q21.1
A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: fibrillin; EGF homology
C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; F;1-3002/Product: fibrillin (5'-region exon A splice form) #status predicted <MATC>
F;1332-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
F;1332-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
F;1457-1492/Domain: EGF homology <EGF2>
F;2262-2295/Domain: EGF homology <EGF1>

381 HEPHRCQFNCQTACPADCDNTQAS--CECEGVILDDGFICTDIDEC-EN----- 429
1500 NGTHWCSOH-----ADC-KNTWGSYRLCKEY--TGDGFTCTDLDECSENLCNGQ 1550
430 -----GGF-----CS-----GVCHNLPGTFECICGPDLSALA 455
1551 CLNAPGYRCECDMGFVPSADGKACEDIDCSLPLNLCVFGTCHNLPGFRCCECEGYELD 1610
456 RHIG-----TDCDSGVKVDGSSGEPSPPTGS-----TLTPPAVGLV 495
1611 RSGNCTDNECLDPTTCISGNCVN-----TPGSYICDPPDFELNPTRVGCV 1658
RESULT 11
ASS624
fibrillin-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 24-Nov-2003
C;Accession: A55624
R;fin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene.
A;Reference number: A55624; MUID:95130561; PMID:7829516
A;Accession: A55624
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <VIN>
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C;Genetics:
A;Gene: Fbn-1
C;Superfamily: fibrillin; EGF homology
F;1201-1236/Domain: EGF homology <EGF>
Query Match 12.8%; Score 362; DB 2; Length 2871;
Best Local Similarity 29.4%; Pred. No. 3.7e-14;
Matches 117; Conservative 26; Mismatches 127; Indels 128; Gaps 21;
194 SAAVAPLGL-----QLMCTAPPAGVQGHVAREAPAGWDCSVENGCGCHACNAIPGAPRC 247
1162 SANLPHRCVNLGKYOCACNPGVPHTRDLFCVDIDECIMNGGCTFTCTNSDGYEC 1221
248 QCPAALQADGRSTASATOSCNLDCEHFCVNP-----DQGSYSQMCETGYRL 298
1222 SCQPFALMPDQSC-----DIDQ--CEDNPNICDGGCTNIPREYRLCYDGFNA 1271
299 ADQHRCEVDVDCILEPSPC-PQRCVNTQGGPECHYFNIDVDBE--CPEVDPC--FR 353
1272 SEDMTKVDVNECDLNPICLSGTCTENTKGSFICHCDMGYSKKGKTGCTD-INECEIGA 1330
354 ANCEYQCOPLNOT-SYLCVCAEGFA-----PIPEHRCQFNCQTACPADCDN 402
1331 HNGRHAHVCTNTAGSKFCSCSPGWIGDKIKTDLDECSTNGTHMCSQH-----ADC-KN 1382
403 TQAS--CECEGVILDDGFICTDIDEC-EN-----GGF----- 432
1383 TMGSYRLCKOGY--TGDGFTCTDLDECSENLCNCGQCLNAPGGYRCDCMGFVPSADG 1441
433 -----CS-----GVCHNLPGTFECICGPDLSALRHIG-----TDCDSGK 466
1442 KACEDIDCSLPLNLCVFGTCHNLPGFRCCECEGYELDRSGNCTDNECLDPTTCISGN 1501
467 VDGDSGSGEPSPPTGS-----TLTPPAVGLV 495
1502 CVN-----TPGSYICDPPDFELNPTRVGCV 1527
RESULT 12
T46488
hypothetical protein DKFZp434J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46488

Query Match 12.9%; Score 364; DB 2; Length 3002;
Best Local Similarity 30.8%; Pred. No. 2.9e-14;
Matches 111; Conservative 22; Mismatches 105; Indels 122; Gaps 20;
226 DCSVENGGCEHACNAIPGAPRCQCPAGALQADGRSTASATOSCNLDCEHFCVNP--- 282
1331 ECSIMNGGCEFTCTNSGSEYSCSPGALMPDQSC-----DIDE--CEDNPNIC 1380
283 -----DQGSYSQMCETGYRLADQHRCEVDVDCILEPSPC-PQRCVNTQGGPECHCYP 335
1381 DGGQCTNIPGEYRLCYDGFNAWSEDMTKVDVNECDLNPICLSGTCTENTKGSFICHDM 1440
336 NYDLVDGE--CPEVDPC--FRANCEYQCOPLNOT-SYLCVCAEGFA-----PIP 380
1441 GYSKKGKGTGCTD-INECEIGHNCGKHAHVCTNTAGSKFCSCSPGWIGDKIKTDLDEC 1499

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23035
A;Accession: T46488
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: EMBL:AL137638
A;Experimental source: adult testis; clone DKFZp434J065
C;Genetics:
A;Note: DKFZp434J065.1

Query Match	12.6%	Score 357;	DB 2;	Length 741;
Best Local Similarity	31.6%	Pred. No. 2.5e-14;		
Matches	86;	Conservative	40;	Mismatches 102; Indels 44; Gaps 15;
227	CSVENGCEHA	CNAIPGAP	CCQCPAGA	LQADGRSCTA-SATQSCNDLCHEHFCVNPPOOP 285
	: :	: :	: :	: :
68	CAMEDHNC	EQCLCVN	VPFSFVCQ	SYGALAEGRKCVAVDYCASENHGECHV-NAD-- 124
	: :	: :	: :	: :
286	GSYSQMC	GTGYRLA	ADHRCE	VDVDCILEPSPCPQRCVNTQGGFFCHCVNYDL-VDGEC 344
	: :	: :	: :	: :
125	GSYLQCH	EGFALN	DEKTCIK	IDYCASSNHGCHCVNTDSDSYSCHLKGFTLPDKKT 184
	: :	: :	: :	: :
345	VEPVDPCF	--RANCY	QOQPLN	QTSYLCVACGFPAPIPH-----EPHRCOMFC 390
	: :	: :	: :	: :
185	CRINVCAL	NKPGCE	HECVNMEE	-SYICRCHRGYTLDPNGKTCRVDHCAQQHGEQJLC 243
	: :	: :	: :	: :
391	NOTACPAD	CDPNTQAS	--CECEP	EYTLDDGF-ICTDIDEC---ENGFGCSGVCHNLPGTF 444
	: :	: :	: :	: :
244	-----	LNTEDS	FVCQCS	EGFLINDELKTCRSDYVYCLLSDHG--CEYSCVNMDRSF 291
	: :	: :	: :	: :
445	ECICGPD	SALARH	IGTDCD	SGKVDG---GDSG 473
	: :	: :	: :	: :
292	ACQC-PE	GHVLR	SDGKTC	--AKUJSCALGDHG 320
	: :	: :	: :	: :

RESULT 13

A49457

fibulin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-2002

C/Accession: A49457; S74095

R/Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.

J. Cell Biol. 123, 1269-1277, 1993

A/Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with

A/Reference number: A49457; MUID:94064787; PMID:8245130

A/Accession: A49457

A/Status: preliminary

A/Molecule type: MRNA

A/Residues: 1-1221 <PAN>

A/Cross-references: GB:X75285; NID:G437046; PIDN:CAA53040.1; PID:G437047

R/Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A/Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix met

A/Reference number: S74094; MUID:96439073; PMID:8841408

A/Accession: S74095

A/Molecule type: protein

A/Residues: 236-238, 'X', 240-247;260-275;336-344, 'L', 346-361;405-426;566-568, 'EM', 569-589

C/Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C/Keywords: calcium binding; duplication; extracellular matrix; glycoprotein, homotrimer

E.042-974/nomai: EGF homology <EGF>

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Query Match          12.6%; Score 357; DB 2; Length 1221;
Best Local Similarity 29.5%; Pred. No. 3.7e-14;
Matches 123; Conservative 39; Mismatches 141; Indels 114; Gaps 27;

136 EQOCEVKAD-GFLCFHFHPATC-----RPLAV-----EPGAAAAAVS-----IT 174
      ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
521 EGOSCBSENPLGYPCHN-HVMLSCEGEPLIVEVRPPEPEAAAPRVSEMEASREALS 579
      ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
175 YGT-----PFAAGADFQ-----ALP-----VGSSAAVAPLGLQLM-----CTAPPG 211
      ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

580 LGTEAELPNSLPGDDODECLMLPGELCOHLICINTVGSYRCACFPFGFELQGGDRTCRDRG 639

212 AVQGHWARE-APGAWDCSV-----ENGGEHACNAIPGAPRCQCPAGAA 254

640 APOLDTARESPASRESAQVSPNTIPLVPQFNTCKDNGPCQVCRVVGDTAMCSFFGVA 699

255 LQADGRSC-----TASATQSCNDLCBHFCVNPDPQGSYSC-----MCETGYRLAADQHR 304

700 IMADGVSCEDQDECLMTHDCS--WKQFCV---NTLGSFYCVNHTVLCAEGYILNA-ERK 753

305 CEVDVDDCILPSPC--PQRCVNTQGGFECH-----CYPNYDLVDGECVBPVPCFPA--NC 356

754 CVDINECVTLHTCTRAEHCVNTPGSGFCYKALICEPGYVLTGECTD--VDECVTGTTHNC 812

357 E--YQCOPLNQTSVLV-----CAGSFAPIPH-----EPHRCQMFNCNOTACPA 397

813 QAGFSCQN--TKGSFYCAQRCQMDGFLQDPGNCVVDINECTSLLEPCRSFGFSICNTVGSY 871

398 DCDPNTQASCPCPEY-ILDDGFICTDIDECENGGFCSG---VCHNLPOTFEICCP 450

872 TCQRNPLV---CGRGYHANEBSGECVDYNECETGVHRCGEGQLCVNLPGSYRCDCKP 925

RESULT 14

T09059

notch4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002

C:Accession: T09059

R:Rowen, L.; Mahalikas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; SC submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543

A:Accession: T09059

A>Status: preliminary; translated from GB/EMBL/DBDBJ

A:Molecule type: DNA

A:Residues: 1-1964 <ROW>

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C;Genetics:
A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/1
1679/3; 1729/1; 1763/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>

Query Match      11.7%; Score 332.5; DB 2; Length 1964;
Best Local Similarity 25.3%; Pred. No. 1.6e-12;
Matches 128; Conservative 34; Mismatches 142; Indels 183; Gaps 31;

116 GPLCVAVSAARATVPSEFIWEEQCEVKADGFLCE-FHPBPATCRPLAVEPGAAAAVSIT 174
35 GGTCLRLSRGGGIC-----QC--APGFLGETCQFPDPGR----- 66
175 YGTFPAARGADFOAL---PVGSSAAVPLGLQLMCTAPPG---AVQGHWAREAPGAWDC 227
67 -DTQLCKNGSGSCQALLTPPSSRSSTSELTPHFSCTPSGFTGDRCQTHLEELCPSPF-C 124
228 SVENGGECHAGNAIPGAPRCQCPAGAAQLADGRSCATASATQSCNDLCEHFCVNPDPGP- 286
125 S--NGG--HCYVQASGRPQCCEPGWT-----GEQCO-----LRDFCSANPCANGG 166
287 -----SYSCWCETGYRLAADOHRCE-DVDDCILEPSPCPQ--RCVNTQGGFECHC--- 333
167 VCLATYPQIQRCPPGF-----EGHTCERDINECFLEPGFCPQGTSHNTLGSYOCLCEVG 222
334 ---YPNVYDLVDGECVEPVDPCFRANCEYQCOPL---NQTSYLVCVCAEGFAIPHE----- 382
223 QSGFPQCKLRKAC--PPGSCNLGG--TCOLVPEGHSTFHLCLCPGFTGLDCMNPDCC 277
383 -PHRCQMFNQTCAPDADCDNTQASCCEPGYILDDGFICT-DIDICE-----NGGF 432

```

Wed Jun 9 13:16:02 2004

278 VRHQQ---NGATCLDGLDVT---CLCPKW---KWDCESEDIDECEARGPPRCRNGGT 328
433 C-----SGVCHNLPGTFECICGP-----450
329 QNTAGSPHCVCVSGWGAGCEENLDDCAAAATCAPGSTCIDRVGSFSLCPFGRTGLCH 388
451 --DSALAR--HIGTDCDSKVDG-----GDSGS-----GEPPSP-----481
389 LEDMCLSPCHVNAQCSNPLTGSPLCICQPGYSGSTCHQDLDECQMAQQGSPCEHGS 448
482 ---TEGS 485
449 CINTFGS 455

RESULT 15

T43210
fibulin-1D precursor - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002
C:Accession: T43210
R:Barth, J.L.; Argaves, K.M.; Roark, E.F.; Little, C.D.; Argaves, W.S.
A:Description: Identification of chicken and C. elegans fibulin-1 homologs and character
A:Reference number: Z22337
A:Accession: T43210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-589 <BAR>
A:Cross-references: EMBL:AF070477; PIDN:AAC24035.1
C:Genetics:
A:Note: intron positions not resolved (incomplete sequence)
C:Superfamily: fibulin-1; EGF homology

Query Match 11.7%; Score 331; DB 2; Length 589;
Best Local Similarity 28.1%; Pred. No. 7.5e-13;
Matches 126; Conservative 49; Mismatches 166; Indels 108; Gaps 28;
QY 85 GPLRGP-QWVTGDNNTSYSRWARLDLNGAPLCGLCVASAAEATVPSEPI-----WEEQ 138
DB 19 GCLRSFNKCCNGDIEITH---ASEIITGRPLNDPHVLHLGDRCCASSHCEHLCHDRGGKEV 75
QY 139 QCEVKA-----DGFCLCEHFPF--ATCRPLAVE-----PGAAAAVSIYGTPEA--- 180
DB 76 ECSCRSGFDLAPDGNACVDHIDEACATLMDCLCSQRCINTPGSFCKIRTLSCGIGYAMDS 135
QY 181 --ARGADFOALPVGSSAAVAPLGLQIMCTAPPVAVQ-----GHWAREAPGAWDCS----- 228
DB 136 ETERCRDVDECNLGSF-----DCGPLYQCRNTQGSYRCDAKKGDGELQNPMTGECTSITC 191
QY 229 -----VENGGCE-----HACNA-----IPGAPRCQ-----CPAGAALOADGSCCTA 264
DB 192 PNGYYPKNGMCMNDIDECVTGHNCGAGEECVNTPGSFRCQCKGNLCAHYEVN----- 243
QY 265 SATQSCNDL--CEH-----FCVPNDPQGSYSCMCTGYRLAADQHRCEVDVDCIL---- 313
DB 244 GATGFCEDVNECQQGVCGSMCECI---NLPGTYKCKCPGPFENDAKKRCEDVDECIKFAG 300
QY 314 EPSFCPCRCVNTQSGPECHCPYNDLV--DGECEVPVDPQFR--ANCEYQCQPLNOTSILC 370
DB 301 HVCDSLAEBCINTIGSFCECKPGFQLASDGRCEDVNECTTGTAACEQKCVNI--PGSYQC 359
QY 371 VCAEGFAPIP-----HEPHRCQMF--NOTACPADCDPNTQAS--CECPGY-ILDDGFI 420
DB 360 ICDRGFALGPDGDKCEDIDECISIWAGSNDLCMGGC--INTKGYLCCQCPGYKIQPDRT 418
QY 421 CTDIDCEGNGFCSG-----VCHNLPGTFEC 446
DB 419 CVDVDECAMGE-CAGSDKVCVNTLGSFKC 446

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OM protein - protein search, using sw model

Run on: June 9, 2004, 08:42:38 ; Search time 10.5 Seconds
(without alignments)
2469.613 Million cell updates/sec

Title: US-09-509-994-2_COPY_19_516
Perfect score: 2830
Sequence: 1 APAEPQGGSCVHDCFAL.....PSPTFGSLTPPAVGLVHSG 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	100.0	575	1 TRBM_HUMAN	P07204 homo sapien
2	1858	65.7	577	1 TRBM_MOUSE	P15306 mus musculus
3	1095.5	38.7	356	1 TRBM_BOVIN	P06579 bos taurus
4	582	20.6	652	1 CD93_HUMAN	Q9p573 homo sapien
5	542	19.2	644	1 CD93_MOUSE	O89103 mus musculus
6	525.5	18.6	643	1 CD93_RAT	Q9et61 rattus norv
7	374	13.2	2907	1 FN2_MOUSE	P61555 mus musculus
8	368	13.0	2871	1 FN1_BOVIN	P98133 bos taurus
9	367.5	13.0	1184	1 FN2_HUMAN	P98095 homo sapien
10	366	12.9	2911	1 FN1_PIG	Q9tv36 sus scrofa
11	366	12.9	2871	1 FN2_HUMAN	P35556 homo sapien
12	364	12.9	2871	1 FN1_HUMAN	P35555 homo sapien
13	362	12.8	2871	1 FN1_MOUSE	P61554 mus musculus
14	357	12.6	1221	1 FN2_MOUSE	P37889 mus musculus
15	356	12.6	956	1 MTN2_HUMAN	O00339 homo sapien
16	332.5	11.7	1964	1 NTC4_MOUSE	P31695 mus musculus
17	331.5	11.7	1389	1 LTBS_MOUSE	Q8cg18 mus musculus
18	331.5	11.7	1713	1 LTBL_MOUSE	Q8cg19 mus musculus
19	330.5	11.7	1712	1 LTBL_RAT	O0918 rattus norv
20	326.5	11.5	956	1 MTN2_MOUSE	O08746 mus musculus
21	322.5	11.4	1394	1 LTBS_HUMAN	P22064 homo sapien
22	322.5	11.4	1595	1 NTC3_HUMAN	Q14766 homo sapien
23	321	11.3	2321	1 NTC3_HUMAN	Q9um47 homo sapien
24	315.5	11.1	443	1 FN1_HUMAN	O95967 homo sapien
25	313	11.1	798	1 FN1_MOUSE	P23142 homo sapien
26	311	11.0	703	1 FN1_HUMAN	O77469 caenorhabdi
27	308.5	10.9	443	1 FN1_CRIGR	O55058 cricetus
28	308.5	10.9	2003	1 NTC4_HUMAN	Q99466 homo sapien
29	308	10.9	448	1 FN1_HUMAN	Q9ubx5 homo sapien
30	307	10.8	704	1 FN1_CHICK	O73775 gallus gall
31	306.5	10.8	443	1 FN1_MOUSE	Q9wvj9 mus musculus
32	306	10.8	681	1 FN1_BRARE	O42182 brachydanio
33	306	10.8	705	1 FN1_MOUSE	Q08879 mus musculus

34	302	10.7	448	1 FBL5_MOUSE	Q9wvh9 mus musculus
35	297	10.5	2531	1 NTC1_MOUSE	Q01705 mus musculus
36	296	10.5	448	1 FBL5_RAT	Q9wvh8 rattus norv
37	294	10.4	2319	1 NTC3_RAT	Q9rl72 rattus norv
38	292	10.3	2470	1 NTC2_MOUSE	O35516 mus musculus
39	291	10.3	598	1 PBL1_CERAE	Q8mj39 cercopithec
40	289.5	10.2	493	1 FBL3_HUMAN	Q12805 homo sapien
41	287	10.1	2471	1 FBL3_MOUSE	Q9w30 rattus norv
42	285	10.1	2471	1 NTC2_RAT	Q04721 homo sapien
43	284.5	10.1	2437	1 NTC1_HUMAN	P46530 brachydanio
44	280.5	9.9	2703	1 NTC1_BRARE	P07207 drosophila
45	280	9.9	2318	1 NTC3_MOUSE	Q61982 mus musculus

ALIGNMENTS

RESULT 1	TRBM_HUMAN	STANDARD	PRT	575 AA.
ID	P07204			
AC	P07204			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Thrombomodulin precursor (Petomodulin) (TM) (CD141 antigen).			
GN	THBD OR THRM			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88004395; PubMed=2820710;			
RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioka J., Maruyama I.,			
RA	Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.,			
RT	"Structure and expression of human thrombomodulin, a thrombin			
RT	receptor on endothelium acting as a cofactor for protein C			
RT	activation."			
RL	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.,			
RT	"Human thrombomodulin: complete cDNA sequence and chromosome			
RT	localization of the gene."			
RL	Biochemistry 26:4350-4357(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87317665; PubMed=2819876;			
RA	Jackman R.W., Beiler D.B., Fritze L., Soff G., Rosenberg R.D.,			
RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences			
RT	of the cDNA and gene predict protein structure and suggest sites of			
RT	regulatory control."			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88227901; PubMed=2836377;			
RA	Shirai T., Shoji S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.,			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-			
RT	catalyzed activation of protein C."			
RL	J. Biochem. 103:281-285(1988).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Roel C.L., Toth E.J., Yi Q., Nickerson D.A.,			
RA	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguely C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			

Wed Jun 9 13:16:02 2004

- RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clapp M.E., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhama P.D., Dunn M.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Grafham D.V., Griffiths J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammon S., Harley J.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.L., King A., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Lehaeslaio M.A., Martin S.L., McConachie L.J., McLay K., McMurray A.,
RA Marsh V.L., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuie C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RA Nature 414:865-871(2001).
RA [7]
RA SEQUENCE FROM N.A.
RA TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [8]
RA CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
RA MEDLINE=94029900; PubMed=8216207;
RA Gerleitz B., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,
RA Grinnell B.W.;
RA "Identification of the predominant glycosaminoglycan-attachment site
RA in soluble recombinant human thrombomodulin: potential regulation of
RA functionality by glycosyltransferase competition for serine474.";
RA Biochem. J. 295:131-140(1993).
RA [9]
RA STRUCTURE BY NMR OF 389-407.
RA MEDLINE=96007474; PubMed=7559494;
RA Adler M., Seto M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;
RA "The structure of a 19-residue fragment from the C-loop of the fourth
RA epidermal growth factor-like domain of thrombomodulin.";
RA J. Biol. Chem. 270:23366-23372(1995).
RA [10]
RA STRUCTURE BY NMR OF 364-407.
RA MEDLINE=96100636; PubMed=8528067;
RA Meininger D.P., Hunter M.J., Komives E.A.;
RA "Synthesis, activity, and preliminary structure of the fourth
RA EGF-like domain of thrombomodulin.";
RA Protein Sci. 4:1693-1695(1995).
RA [11]
RA STRUCTURE BY NMR OF 427-444.
RX MEDLINE=95034791; PubMed=7947766;
RX Sinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
RX "Thrombin-bound structure of an EGF subdomain from human
RX thrombomodulin determined by transferred nuclear Overhauser
RX effects.";
RX Biochemistry 33:13553-13560(1994).
RX [12]
RX STRUCTURE BY NMR OF 427-444.
RX MEDLINE=96276211; PubMed=8745396;
RX Hrabal R., Komives E.A., Ni F.;
RX "Structural resiliency of an EGF-like subdomain bound to its target
RX protein, thrombin.";
RX Protein Sci. 5:195-203(1996).
RX [13]
RX STRUCTURE BY NMR OF 405-444.
RX MEDLINE=98035729; PubMed=9367781;
RX Sampoli Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;
RX "Structure of the fifth EGF-like domain of thrombomodulin: an
RX EGF-like domain with a novel disulfide-bonding pattern.";
RX J. Mol. Biol. 273:913-926(1997).
RX [14]
RX VARIANT TED TYR-486.
RX MEDLINE=95111115; PubMed=7811989;
RX Oehlin A.-K., Marlar R.A.;
RX "The first mutation identified in the thrombomodulin gene in a
RX 45-year-old man presenting with thromboembolic disease.";
RX Blood 85:330-336(1995).
RX [15]
RX VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.
RX MEDLINE=97341986; PubMed=9198186;
RX Oehlin A.-K., Norlund L., Marlar R.A.;
RX "Thrombomodulin gene variations and thromboembolic disease.";
RX Thromb. Haemost. 78:396-400(1997).
RX [16]
RX VARIANT VAL-473.
RX MEDLINE=97206518; PubMed=9157575;
RX Norlund L., Holm J., Zoller B., Oehlin A.-K.;
RX "A common thrombomodulin amino acid dimorphism is associated with
RX myocardial infarction.";
RX Thromb. Haemost. 77:248-251(1997).
RX [17]
RX VARIANT THR-43.
RX MEDLINE=99057299; PubMed=9843165;
RX Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
RX Stubgen P.J., Manger Cats V., Ireland H.;
RX "A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,
RX and the risk of myocardial infarction in men.";
RX Thromb. Haemost. 80:743-748(1998).
RX [18]
RX VARIANT VAL-473.
RX MEDLINE=21143723; PubMed=11245641;
RX Wu K.K., Aleksic N., Ahn C., Boerwinkle E., Folsom A.R.,
RX Juneja H.;
RX "Thrombomodulin Ala455Val polymorphism and risk of coronary heart
RX disease.";
RX Circulation 103:1386-1389(2001).
RX [19]
RX VARIANT TED TYR-486, AND VARIANT VAL-473.
RX MEDLINE=22135346; PubMed=12139752;
RX Faioni E.M., Franchi F., Castaman G., Biguzzi E., Rodeghiero F.;
RX "Mutations in the thrombomodulin gene are rare in patients with
RX severe thrombophilia.";
RX Br. J. Haematol. 118:595-599(2002).
RX -!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
RX that forms a 1:1 stoichiometric complex with thrombin. This
RX complex is responsible for the conversion of protein C to the
RX activated protein C (protein Ca). Once evolved, protein Ca
RX scissions the activated cofactors of the coagulation mechanism,
RX factor Va and factor VIIIa, and thereby reduces the amount of
RX thrombin generated.
RX -!- SUBCELLULAR LOCATION: Type I membrane protein.
RX -!- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
RX thrombomodulin.

FT	CARBOHYD	408	408	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	494	494	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).	
SEQ	SEQUENCE	577 AA;	61867 MW;	B20E50B0FE745014 CRC64;	
Query Match					
Best Local Similarity 65.7%; Score 1858; DB 1; Length 577;					
Matches 332; Conservative 45; Mismatches 118; Indels 8; Gaps 4;					
Qy	1	APAPQGGSCQVEHDCFALYPGPATFALNASQICDGLRGLHMTVRSSVAADVISLLNGD	60		
Db	19	ALAKLQTSQCVHEHCFALFQGPATFELDASQACORLQGLHMTVRSSVAADVISLLSQS	78		
Qy	61	G-GVRRRLMIGLQPLPGCGDKPKLPLRGFWTGTGNTSYSHWARLDLNGALCPGLC	119		
Db	79	SMDLGP---WIGLQLOQCDPDVHLGRLRGFWTGTGNTSYSHWARLPDQATPLOGPLC	135		
Qy	120	VAVSAAEATVSEPIWEEQCEKADGFLCEFFHPPATCRPLAVEP-GAAAAAASVITYGTP	178		
Db	136	VTVSTAEATGEPAWEKPCETETQFLCEFFYFTASCRPLTVNTRDPEAAHISSTYNTP	195		
Qy	179	FAARGADPQALPVGSSAAVPLGLQLMCTAPPAGVQGHWAREAPGAWDCSVENGCSHAC	238		
Db	196	FGVSGADFQTLVPVGSSAAVEPLGLELCRAPPGTSEGHWAREATGAWNCVSENGCCEYL	255		
Qy	239	NAIPGAPRCQCPAGNALQADGSCSTASATQSCNDLCEHFCVNPDPQSGSYSCMCTGYRL	298		
Db	256	NRSTNEPRCLCPDMDLQADGSCCARPVVQSCNELCEHFCVNSAEVPGSYSCMCTGYQL	315		
Qy	299	AADHRCEDVDCCILEPSPQPCQRCVNTGGGCEHCYNYDLVDGCEVPEVPDPFRANCEY	358		
Db	316	AADGHRCEVDVDCQKQGNPCQLCVNTKGFECECYDGYELVDGCEVLLDPCFGSNEF	375		
Qy	359	QCQPLNQTSLYLCVCAEGFAPIPHEPHRCMPCNCTACPADCDPNTQASCECPGVIYLDG	418		
Db	376	QCQVSPDYRCICACGAPKAPKPEPHKCEMFCNETSCPADCDPNSPTVCECPGFIIDEG	435		
Qy	419	FICTDIDCEGNGGFCGCHNLPGTFECICGPDASALARIHGTDCDSGKV---DGDGSGG	475		
Db	436	SVCTDIDSCSGCEFTSECRNPPGSEYICIGPDTHALAQISKDCDPIPVREDTKEEGSG	495		
Qy	476	EPSPPTPGSTLTPPAVGLVHSG 498			
Db	496	EPVSPPTGSPGTPSPARPVHSG 518			
RESULT 3					
TRBM	BOVIN	STANDARD;	PRT;	356 AA.	
ID	TRBM	BOVIN			
AC	P06579;				
DT	01-JAN-1988	(Rel. 06, Created)			
DT	01-JAN-1988	(Rel. 06, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Thrombomodulin (fetomodulin) (TM) (Fragment).				
GN	THBD.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RP	SEQUENCE FROM N.A.				
EX	MEDLINE=67067408; PubMed=3024152;				
RA	Jackman R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;				
RT	"Characterization of a thrombomodulin cDNA reveals structural				
RT	similarity to the low density lipoprotein receptor."				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8834-8838 (1986).				
CC	-!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor				
CC	that forms a 1:1 stoichiometric complex with thrombin. This				
CC	complex is responsible for the conversion of protein C to the				
CC	activated protein C (protein Ca). Once evolved, protein Ca				
CC	scissions the activated cofactors of the coagulation mechanism,				
CC	factor Va and factor VIIIa, and thereby reduces the amount of				

CC	thrombin generated.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing				
CC	thrombomodulin.				
CC	-!- SIMILARITY: Contains 6 EGF-like domains.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
EMBL	M14657; AAA30785.1; --				
PIR	A25918; A25918.				
HSSP	P07204; 1TMR.				
DR	InterPro; IPR000152; Asx hydroxyl_s.				
DR	InterPro; IPR001881; EGF_Ca.				
DR	InterPro; IPR006209; EGF-like.				
DR	InterPro; IPR001491; Thrombomodulin.				
DR	Pfam; PF00008; EGF_4.				
DR	PRINTS; PR00907; THROMBOMODULIN.				
DR	SMART; SM00179; EGF_CA; 1.				
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.				
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.				
DR	PROSITE; PS01186; EGF_2; 3.				
DR	PROSITE; PS00026; EGF_3; 3.				
DR	PROSITE; PS01187; EGF_CA; 2.				
KW	Endothelial cell; Receptor; Blood coagulation; Repeat; Transmembrane;				
KW	Glycoprotein; EGF-like domain.				
FT	NON TER 1 1				
FT	DOMAIN 1 296				
FT	TRANSMEM 297 320				
FT	DOMAIN 321 356				
FT	DOMAIN 17 57				
FT	DOMAIN 60 98				
FT	DOMAIN 99 137				
FT	DOMAIN 139 179				
FT	DOMAIN 178 214				
FT	DOMAIN 215 254				
FT	DISULFID 21 32				
FT	DISULFID 28 41				
FT	DISULFID 43 56				
FT	DISULFID 64 72				
FT	DISULFID 68 82				
FT	DISULFID 84 97				
FT	DISULFID 103 114				
FT	DISULFID 110 123				
FT	DISULFID 125 136				
FT	DISULFID 143 152				
FT	DISULFID 148 162				
FT	DISULFID 164 178				
FT	DISULFID 182 191				
FT	DISULFID 187 199				
FT	DISULFID 201 213				
FT	DISULFID 219 228				
FT	DISULFID 224 237				
FT	DISULFID 239 253				
FT	CARBOHYD 271 271				
SEQ	SEQUENCE 356 AA; 37795 MW; 29841F097ABE1093 CRC64;				
Query Match					
Best Local Similarity 38.7%; Score 1095.5; DB 1; Length 356;					
Matches 189; Conservative 31; Mismatches 63; Indels 15; Gaps 6;					
Qy	211	GAVQGHWAREAPGAWDCSVENGCGHACNAIPGAPRCQCPAGALQADGRSTASATQSC	270		
Db	5	GTEGWSREAPGAWACGVGGCQCKGAGASNCCLCPADALQADGRSCGLPAEHPC	64		
Qy	271	NDLCHEFCVNPDPQSGSCMCTGYRLAADHRCEDVDCCILEPSPQPCQRCVNTQSGFE	330		

"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
[4]
SEQUENCE FROM N.A.
STRausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J.G., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RESULT 4

[5] CHARACTERIZATION.
MEDLINE=21990337; PubMed=11994479;
McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.;
"Human C1qRp is identical with CD93 and the mNI-11 antigen but does
not bind C1q";
J. Immunol. 168:5222-5232(2002).

[6] O-GLYCOSYLATION
MEDLINE=99192777; PubMed=10092817;
Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;
"C1qRp is a heavily O-glycosylated cell surface protein involved in
the regulation of phagocytic activity";
J. Immunol. 162:3583-3589(1999).

-- FUNCTION: Receptor (or element of a larger receptor complex) for
C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
protein A (SPA). May mediate the enhancement of phagocytosis in
monocytes and macrophages upon interaction with soluble defense
collagens. May play a role in intercellular adhesion.

-- SUBCELLULAR LOCATION: Type I membrane protein.

-- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
platelets, cells of myeloid origin, such as monocytes and
neutrophils. Not expressed in cells of lymphoid origin.

-- PTM: N- and O-glycosylated.

-- SIMILARITY: Contains 1 C-type lectin family domain.

-- SIMILARITY: Contains 5 EGF-like domains.

-- CAUTION: Has been sometimes referred to as a collectin receptor.

-- CAUTION: According to Ref.5, C1q is not a ligand for C1qR1.

-- DATABASE: NAME=NCBI; NOTB=PROW 3:1-6(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456.g.htm".

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or send an email to license@isb-sib.ch).

EMBL; U94333; AAB53110.1; --
EMBL; AL118508; CAC00597.1; --
EMBL; BC028075; AAB28075.1; --
HSP; P35555; 1EMN.
Genew; HGNC:15855; C1QR1.
MIM; 120577; --
GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0004872; F:receptor activity; NAS.

DR GO: 0016337; P: cell-cell adhesion; IDA.
 DR GO: 0042116; P: macrophage activation; NAS.
 DR GO: 0006909; P: phagocytosis; NAS.
 DR InterPro: IPR00152; Aex hydroxylase.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00008; EGF; 5.
 DR Pfam: PF00059; Lectin_C; 1.
 DR SMART: SM00334; CLECT; 1.
 DR SMART: SM00179; EGF_Ca; 3.
 DR PROSITE: PS00010; AEX_HYDROXYL; 3.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
 DR PROSITE: PS01186; EGF; 2; 3.
 DR PROSITE: PS00026; EGF; 3; 3.
 DR PROSITE: PS01187; EGF_Ca; 3.
 DR Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein; Polymorphism.
 KW SIGNAL
 FT CHAIN 22 652
 FT DOMAIN 24 580
 FT TRANSMEM 581 601
 FT DOMAIN 602 652
 FT DOMAIN 32 174
 FT DOMAIN 360 301
 FT DOMAIN 302 344
 FT DOMAIN 345 384
 FT DOMAIN 385 426
 FT DOMAIN 427 468
 FT DOMAIN 594 601
 FT DISULFID 264 275
 FT DISULFID 271 285
 FT DISULFID 287 300
 FT DISULFID 306 317
 FT DISULFID 311 328
 FT DISULFID 330 343
 FT DISULFID 349 358
 FT DISULFID 354 367
 FT DISULFID 369 383
 FT DISULFID 389 400
 FT DISULFID 396 409
 FT DISULFID 411 425
 FT DISULFID 431 443
 FT DISULFID 439 452
 FT DISULFID 454 467
 FT CARBOHYD 325 325
 FT VARIANT 318 318
 FT CONFLICT 22 22
 FT CONFLICT 36 36
 FT CONFLICT 38 39
 FT CONFLICT 155 155
 FT CONFLICT 186 186
 FT CONFLICT 492 492
 FT CONFLICT 496 496
 FT CONFLICT 504 504
 FT CONFLICT 541 541
 FT CONFLICT 541 541
 FT CONFLICT 652 AA; ECA0FEAC55FCAC2 CRC64;
 Query Match 20.6%; Score 582; DB 1; Length 652;
 Best Local Similarity 31.8%; Pred. No. 1.4e-31;
 Matches 176; Conservative 52; Mismatches 200; Indels 126; Gaps 31;
 6 QPGGSGQ-----CUEHDCALYPPGATFLNASQICDGLRGLMTVRSSVAD-----VI 53
 17 QPCAGTGADTEAVVCGTACTYATKSAEAAQNHQNGNGLATVSKAEAQHVRL 76
 54 SLILNGDGGVGR--RLWTGLQLPPG-CGDKELGLRGLFQWVTDNNTSYSRWARLDLN 110
 77 AQLRREALTARMSFWLIGLQREKCKLDPSL--FLKGFSSWGGEDTPYSNWKELRN 134
 111 GPLCGLCLCA--VSAAEATVPSE-PIWEEQQ-----EVKADGFLCBFFHPATCRPLA 161

Db 135 SC--ISKRCVSLLLDLSQPLPSRLPKNKGPGSGSPGSGNIEGFVKESFKMGCEPLA 192
 QY 162 V-EPGAAAAVSYTYGTPFAAGADFOALPVGSSAAVPIGLQLMC-TAPPGAVQGHW-- 217
 Db 193 LGGPG-----QVYTTPTQTSSLEAVPFASANVA-----CGEGDKDETQSHYFL 239
 QY 218 -AREAPGAND-----CSVENGGCEHAC-NAIPGAPRCQCPAGAAALQADGRS 261
 Db 240 CEKAPDFVDMGSSGSLVSPKYGCMFNNGGCHQDCPEGGDGSFLGCRPGFRLDLVT 299
 QY 262 CTASATQSCNDLCE--HFCVNPDPQPSYSYSCMCETGYRLAADQHRCEVDVDCILFSPCP 319
 Db 300 C-ASRNPCSSPCGGATCVLGP-HGKNYTCRCPOGVQLDSSQLDQVDVDEC-QDSPCA 355
 QY 320 QRCVNTQGGPECHYNYDVLVDGCEVPEVDPDFRANCEYOCQPLNQTSLCYCAEGFAP 379
 Db 356 QECVNTPGGFRCEWVG-----EPGGP-----GEGACQDVDE-----CALGRSP- 395
 QY 380 PHEHRCQMECNOTACPADCDENTQAS--CECPGYL--DDGFICTDIDEC--ENGDFC 433
 Db 396 -----CAQGC-TWTDGSHCSCEGVVLAGEGTQCCQDVCEVCGPGPLC 439
 QY 434 SGVCHNLGTFECICGPDSSALARHIGTDCDSKV-----DGDGSGSGE-----P 477
 Db 440 DSLCFNTQGSFHGCLGVLAPN-GVSCCTMGVSLGPPSGPDEEDKGEKGSVTPEAA 498
 QY 478 PPSPTPGSTLTPPA 491
 Db 499 TASPTRGPEGTPKA 512
 RESULT 5
 CD93_MOUSE
 ID CD93_MOUSE STANDARD; PRT; 644 AA.
 AC O89103;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q
 DE subcomponent, receptor 1) (C1qrp) (C1qrp(p)) (C1q/MBL/SPA receptor)
 DE (CD93 antigen) (Cell surface antigen AA4) (lymphocyte antigen 68).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=20528605; PubMed=11074255;
 RA Kim T.S., Park M., Nepomuceno R.R., Palmarini G., Winokur S.,
 RA Cotman C.A., Bengtsson U., Tenner A.J.;
 RT "Characterization of the murine homolog of C1qR(P): identical cellular
 RT expression pattern, chromosomal location and functional activity of
 RT the human and murine C1qR(P).";
 RL Mol. Immunol. 37:377-389(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukemia;
 RX MEDLINE=99330438; PubMed=10403644;
 RA Petrenko O., Beavis A., Klaine M., Kittappa R., Godin I.,
 RA Lemischka I.R.;
 RT "The molecular characterization of the fetal stem cell marker AA4";
 RL Immunity 10:691-700(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv; TISSUE=Endothelial cells, and Spleen;
 RX MEDLINE=99359842; PubMed=10430665;
 RA Norworthy P.J., Taylor P.R., Walport M.J., Botta M.;
 RT "Cloning of the mouse homolog of the 126-kDa human C1q/MBL/SP-A
 RT receptor, C1qRp.";
 RL Mamm. Genome 10:789-793(1999).

CC -- FUNCTION: Receptor (or element of a larger receptor complex) for
 CC C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
 CC protein A (SPA). May mediate the enhancement of phagocytosis in
 CC monocytes and macrophages upon interaction with soluble defense
 CC collagens. May play a role in intercellular adhesion. Marker for
 CC early multipotent hematopoietic precursor cells. May play a role
 CC in cell-cell interactions during hematopoietic and vascular
 CC development.

CC -- SUBCELLULAR LOCATION: Type I membrane protein.

CC -- TISSUE SPECIFICITY: Expressed in lung, heart and bone marrow.
 CC Expressed at lower level in ovary, whole embryo and fetal liver.
 CC Not detected in brain, adult liver or thymus. Highly expressed in
 CC peritoneal cavity and bone marrow macrophages. Not detected in
 CC epithelial cells.

CC -- DEVELOPMENTAL STAGE: First detectable in day 9 embryos, in the
 CC endocardium and vascular endothelium in the anterior part of the
 CC embryo. Expression in endothelial cells, initially restricted to
 CC aorta, omphalomesenteric and umbilical arteries, later extends to
 CC subcardinal veins, intersomitic arteries and perimeural vessels.
 CC On day 10, detectable in the entire embryo.

CC -- PTM: N- and O-glycosylated (By similarity).

CC -- SIMILARITY: Contains 1 C-type lectin family domain.

CC -- SIMILARITY: Contains 5 EGF-like domains.

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CC -----

CC ENBL; AF074856; AAC63274.1; -
 CC ENBL; AF081789; AAC62849.1; -
 CC ENBL; AF099339; AAD47906.1; -
 CC ENBL; AF099338; AAD47906.1; JOINED.
 CC HSSP; P35555; IEMN.
 CC MGD; MGI:106664; Clqrl.
 CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0004872; F:receptor activity; ISS.
 CC GO; GO:0016337; P:cell-cell adhesion; ISS.
 CC GO; GO:0042116; P:macrophage activation; ISS.
 CC GO; GO:0006909; P:phagocytosis; ISS.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR001304; Lectin_C.
 CC Pfam; PF00008; EGF; 5.
 CC Pfam; PF00059; lectin_c; 1.
 CC SMART; SM00179; EGF_CA; 3.
 CC SMART; SM00034; CLCCT; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 3.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 CC PROSITE; PS01186; EGF_2; 3.
 CC PROSITE; PS50026; EGF_3; 4.
 CC PROSITE; PS01187; EGF_CA; 3.
 CC Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 CC EGF-like domain; Lectin; Glycoprotein.
 CC SIGNAL 1 22
 CC CHAIN 1 22
 CC DOMAIN 23 644
 CC DOMAIN 23 572
 CC TRANSMEM 573 593
 CC DOMAIN 594 644
 CC DOMAIN 31 173
 CC DOMAIN 257 298
 CC DOMAIN 299 341
 CC DOMAIN 342 381
 CC DOMAIN 382 423
 CC DOMAIN 424 465
 CC DISULFID 261 272

CC BY SIMILARITY.

FT DISULFID 268 282 BY SIMILARITY.
 FT DISULFID 284 297 BY SIMILARITY.
 FT DISULFID 303 314 BY SIMILARITY.
 FT DISULFID 308 325 BY SIMILARITY.
 FT DISULFID 327 340 BY SIMILARITY.
 FT DISULFID 346 355 BY SIMILARITY.
 FT DISULFID 351 364 BY SIMILARITY.
 FT DISULFID 366 380 BY SIMILARITY.
 FT DISULFID 386 397 BY SIMILARITY.
 FT DISULFID 393 406 BY SIMILARITY.
 FT DISULFID 408 422 BY SIMILARITY.
 FT DISULFID 428 440 BY SIMILARITY.
 FT DISULFID 436 449 BY SIMILARITY.
 FT DISULFID 451 464 BY SIMILARITY.
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 644 AA; 69354 MW; EB4351648BF8635A CRC64;
 Query Match 19.2%; Score 542; DB 1; Length 644;
 Best Local Similarity 30.1%; Pred. No. 6.3e-29;
 Matches 160; Conservative 53; Mismatches 199; Indels 120; Gaps 25;
 QY 12 CUEHDCFALYGPATFLNRSQICDGLRHLMTVRSVAA-----DIVISLLNGDGGVGR- 66
 DB 30 CEGTACTYAHWGKLSAAEAQHRCNENGNGNLATYKSEEARHVQOALTLTKAPLEAKM 89
 QY 67 -RLWIGLQLPPGCGDPKRLGRLGFOWVTGDNNISYSRWARLDLNGAPLCGLCAVSA 125
 DB 90 GKFWIGLOREKNCYHDL-FNRGFSWVGGEDTAYSNYKASKSCIFKRCVSLILDLS 148
 QY 126 EATVPEE-PIWEEQQCEV-----KADGFLCFHFHFPATCRPLAV-BPGAAAAVSYTYGT 177
 DB 149 LTPHPSHLPKWHESPCTPEAPGNSTIEGFLCFKFNKMCRLPLALGGFG-----RVITYT 202
 QY 178 PFNARCAQFQALPVGSSAAVAPLGLQ-----LMCT-APRGAVQGHWAREAP-----GAW 225
 DB 203 PFQATTSSLEAVPFASVANVA-CGDEAKSETHYFLCNKTPGIF--HWSSGGLCVSPKF 259
 QY 226 DCSVENGGCGEHAC-NAIPGAPRCQCPAGAAQADGRSCTASATQSCNDLCEHFCVFNPDQ 284
 DB 260 GCSFNGGQQDCFEFGDGSFRGCGPFRLLDLDTVCAS-----RNPSSNPCT 309
 QY 285 PG-----SYSCMCTGYRLAADQHRCEVDVDCILEPSPCPORCVNTQGGFECHY 334
 DB 310 GGMCHSVPLSENITCRCPGQYOLDSSQVHCVDIDEC--QDSPCAQDCVNTLGSFHCEW 367
 QY 335 PNYDLVDG--ECVEPVDPFCFRANCEVQCPQLNQTSLVLCVCAEGEAFIPHEPHRCQMFEN 391
 DB 368 VGIQ-PSGPKKEACEDVDECAANSP-----CAQCCI----- 398
 QY 392 QTACPADCDPNTQAS--CECPGYIL--DDGFICTDIDECEN--GGFCSGVCHNLPTTFE 445
 DB 399 -----NTDGSFYCSCKEYIVSGEDSTOCEDIDECSDARGNCPDCSLCFTNDGSPR 448
 QY 446 CIGPDSALARIHGTDCDSG-----KVDGDSGSGEPSPPTGS 485
 DB 449 CGCPPGWELAPN-GVFCSRGTVFSELPARPQKEDNDRKXESTMPTTEPSS 499
 RESULT 6
 ID CD93_RAT STANDARD; PRT; 643 AA.
 AC Q9ETG1; Q9JIZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q
 DE subcomponent, receptor 1) (ClqRp) (ClqR(p)) (Clq/MBL/SPA receptor)
 DE (CD93 antigen) (Cell surface antigen AA4).
 GN ClQR1 OR CD93 OR ClQR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PVG; TISSUE=Natural killer cells;
 RX MEDLINE=20545218; PubMed=11093152;
 RA Lovik G., Vaage J.T., Dissen E., Spierer C., Ryan J.C., Rolstad B.;
 RT "Characterization and molecular cloning of rat ClqR, a receptor on NK
 cells.";
 RL Eur. J. Immunol. 30:3355-3362(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Lung;
 RX MEDLINE=20507883; PubMed=10934210;
 RA Dean Y.D., McGreal E.P., Akatsue H., Gasque P.;
 RT "Molecular and cellular properties of the rat A4 antigen, a C-type
 lectin-like receptor with structural homology to thrombomodulin.";
 RL J. Biol. Chem. 275:34382-34392(2000).
 CC -|- FUNCTION: Receptor (or element of a larger receptor complex) for
 CC Clq, mannose-binding lectin (MBL2) and pulmonary surfactant
 CC protein A (SPA). May mediate the enhancement of phagocytosis in
 CC monocytes and macrophages upon interaction with soluble defense
 CC cells. May play a role in intercellular adhesion.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and
 CC heart. Expressed at lower level in brain, thymus, liver, spleen,
 CC intestine, kidney, adrenal gland, muscle and testis. Expressed on
 CC endothelial cells, platelets, undifferentiated monocytes and
 CC circulating natural killer cells.
 CC -|- SIMILARITY: Contains 5 EGF-like domains.
 CC -|- SIMILARITY: Contains 5 EGF-like domains.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF136537; AAG01572.1; -;
 DR HGSP; AF160978; AAF80402.1; -;
 DR HSP; P35555; 1EMN.
 DR GO; GO:0016021; C: integral to membrane; ISS.
 DR GO; GO:0004872; F: receptor activity; ISS.
 DR GO; GO:0016337; P: cell-cell adhesion; ISS.
 DR GO; GO:0042116; P: macrophage activation; ISS.
 DR GO; GO:0006909; P: phagocytosis; ISS.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 643
 FT DOMAIN 24 571
 FT TRANSMEM 572 592
 FT DOMAIN 593 643
 FT DOMAIN 31 173
 FT DOMAIN 257 298
 FT DOMAIN 299 341
 FT DOMAIN 342 381
 FT EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 382 423
 FT DOMAIN 424 462
 FT DISULFID 261 272
 FT DISULFID 268 282
 FT DISULFID 284 297
 FT DISULFID 303 314
 FT DISULFID 308 325
 FT DISULFID 327 340
 FT DISULFID 346 355
 FT DISULFID 351 364
 FT DISULFID 366 380
 FT DISULFID 386 397
 FT DISULFID 393 406
 FT DISULFID 408 422
 FT DISULFID 428 437
 FT DISULFID 433 446
 FT DISULFID 448 461
 FT CARBOHYD 322 322
 FT CARBOHYD 498 498
 FT CARBOHYD 417 417
 FT CONFLICT 417 417
 FT SEQUENCE 643 AA; 68781 MW; 9AE4C933AD943DB6 CRC64;
 SQ
 Query Match 18.6%; Score 525.5; DB 1; Length 643;
 Best Local Similarity 30.1%; Pred. No. 7.8e-28;
 Matches 160; Conservative 53; Mismatches 196; Indels 123; Gaps 27;
 QY 12 CVEHDCFALYPPATFLNASQICDGLRGLHMTVRSSVAA-----DVISLLLN-----GDGGV 63
 Db 30 CEGTACTYAHWGKLSAAEAQHRCNENGNLAVYKSEEARHVOEAQLKTKAPSETKI 89
 QY 64 GRRLWIGLQLPPGCGDKPKRLGRLGFQWVTGDNNTSYSRWARLDLNG--APUCGPLCVA 121
 Db 90 G--KFWIGLQREKKGKCTYHDL-PMKGFVWGGEDITTSNWKYKASKSSCIKXCVSLILD 146
 QY 122 VSAEATVSE--PIWEEQCEV-----KADGPLEFHPATCRPLAV-EPGAAAVSI 173
 Db 147 LSLKPH--PSHLPMHESPCGTPDAPGNSIEGFLKFNFKMGCSPLALGGPG-----QL 198
 QY 174 TYGTPEAARGADFOALPVGSSAAVAPLGLQ-----LMCTAPPGAVQGHWAREAP--- 222
 Db 199 TYTTPQATSSLKAVFFASVANV--CGDEAKTNYLYCKETAGV-FHWGSSGLCVS 256
 QY 223 GAWDCSVENGCGCEHAC-NAIPGAPRCQCPAGAAALQADGRSCTASATQSCNDLCEHFCVNP 281
 Db 257 PKFGCSFNNGGCOQDCFEAGDGSFRGCRPGFRLDLDTVCAS-----RNPCCSN 306
 QY 282 PDQPG-----SYSCMCTGYRLADQHRCEVDVDCILLEPSPCPQPCVNTQGGFEC 331
 Db 307 FCTGGGNCVSVLSENYTHCPRGYQLDSSQVHCVDIDEC--EDSPCDQECINTPGGFHC 364
 QY 332 HCYPNYDLVDG--ECVEPVDPCFRANCEYQCQPLNQTSYLCVCAEGFAPIPHEPQRQMF 389
 Db 365 ECWVGQSSGSGKEACEDVDEC-----TAAYSPCAQG----- 396
 QY 390 CNOTACPADCDNPQAS--CECPGKYL--DDGFICTIDECENGFGCSGVCHNLPTTFE 445
 Db 397 CT-----NTDGSFYCSCKEYIMSGEDTQCEDIDEC--LGNPCDTLCINTDGSFR 445
 QY 446 CIGPDSALARHIGTDCDSG-----KVDGDSGSGEPPPTPGS 485
 Db 446 CGCPAGFELAPN-GVSCRTGSMFSELPARPQKEDKDGKSTVPLTEMPGS 496
 RESULT 7
 FB2_MOUSE
 ID FB2_MOUSE STANDARD; PRT; 2907 AA.
 AC Q61555; Q63957;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibrillin 2 precursor.
 GN FB2 OR FB2-2.
 OS Mus musculus (Mouse).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	DOMAIN	1066	1107	EGF-LIKE 15, CALCIUM-BINDING.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	FT	DOMAIN	1108	1150	EGF-LIKE 16, CALCIUM-BINDING.
OX	NCBI_TaxID=10090;	FT	DOMAIN	1151	1192	EGF-LIKE 17, CALCIUM-BINDING.
[1]	SEQUENCE FROM N.A.	FT	DOMAIN	1193	1234	EGF-LIKE 18, CALCIUM-BINDING.
RP	MEDLINE=95263670; PubMed=7744963;	FT	DOMAIN	1235	1275	EGF-LIKE 19, CALCIUM-BINDING.
RX	Zhang H., Hu W., Ramirez F.;	FT	DOMAIN	1276	1317	EGF-LIKE 20, CALCIUM-BINDING.
RA	"developmental expression of fibrillin genes suggests heterogeneity	FT	DOMAIN	1318	1359	EGF-LIKE 21, CALCIUM-BINDING.
RT	of extracellular microfibrils.";	FT	DOMAIN	1360	1400	EGF-LIKE 22, CALCIUM-BINDING.
RL	J. Cell Biol. 129:1165-1176(1995).	FT	DOMAIN	1401	1441	EGF-LIKE 23, CALCIUM-BINDING.
[2]	SEQUENCE OF 210-317 FROM N.A.	FT	DOMAIN	1442	1483	EGF-LIKE 24, CALCIUM-BINDING.
RP	MEDLINE=94140368; PubMed=8307578;	FT	DOMAIN	1484	1524	EGF-LIKE 25, CALCIUM-BINDING.
RX	Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,	FT	REPEAT	1525	1565	EGF-LIKE 26, CALCIUM-BINDING.
RA	Franccke U.;	FT	DOMAIN	1566	1642	TGFBP 4.
RT	"Fibrillin genes map to regions of conserved mouse/human syntenic on	FT	DOMAIN	1643	1684	EGF-LIKE 27, CALCIUM-BINDING.
RL	Genomics 18:667-672(1993).	FT	REPEAT	1685	1726	EGF-LIKE 28, CALCIUM-BINDING.
CC	-I- FUNCTION: Structural component of connective tissue microfibrils	FT	DOMAIN	1727	1800	TGFBP 5.
CC	that binds calcium. Fibrillin-2-containing microfibrils regulate	FT	DOMAIN	1801	1842	EGF-LIKE 29, CALCIUM-BINDING.
CC	the early process of elastic fiber assembly.	FT	DOMAIN	1843	1884	EGF-LIKE 30, CALCIUM-BINDING.
CC	-I- SIMILARITY: Contains 47 EGF-like domains.	FT	DOMAIN	1885	1926	EGF-LIKE 31, CALCIUM-BINDING.
CC	-I- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.	FT	DOMAIN	1927	1965	EGF-LIKE 32, CALCIUM-BINDING.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	FT	DOMAIN	1966	2008	EGF-LIKE 33, CALCIUM-BINDING.
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	FT	DOMAIN	2009	2048	EGF-LIKE 34, CALCIUM-BINDING.
CC	the European Bioinformatics Institute. There are no restrictions on its	FT	DOMAIN	2049	2090	EGF-LIKE 35, CALCIUM-BINDING.
CC	use by non-profit institutions as long as its content is in no way	FT	REPEAT	2091	2163	TGFBP 6.
CC	modified and this statement is not removed. Usage by and for commercial	FT	DOMAIN	2164	2205	EGF-LIKE 36, CALCIUM-BINDING.
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	FT	DOMAIN	2206	2245	EGF-LIKE 37, CALCIUM-BINDING.
CC	or send an email to license@isb-sib.ch).	FT	DOMAIN	2246	2286	EGF-LIKE 38, CALCIUM-BINDING.
CC	EMBL; L39790; AAA74908.1; -;	FT	DOMAIN	2287	2330	EGF-LIKE 39, CALCIUM-BINDING.
DR	EMBL; S63359; AAC60685.1; -;	FT	DOMAIN	2331	2372	EGF-LIKE 40, CALCIUM-BINDING.
DR	PIR; A57278; A57278.	FT	REPEAT	2373	2441	TGFBP 7.
DR	HSP; P35555; 1EMN.	FT	DOMAIN	2442	2483	EGF-LIKE 41, CALCIUM-BINDING.
DR	MGD; GI:95490; Fbn2.	FT	DOMAIN	2484	2524	EGF-LIKE 42, CALCIUM-BINDING.
DR	GO; GO:0030326; P:limb morphogenesis; IMP.	FT	DOMAIN	2525	2563	EGF-LIKE 43, CALCIUM-BINDING.
DR	InterPro; IPR000152; Asx hydroxyl_S.	FT	DOMAIN	2564	2606	EGF-LIKE 44, CALCIUM-BINDING.
DR	InterPro; IPR001881; EGF_Ca.	FT	DOMAIN	2607	2645	EGF-LIKE 45, CALCIUM-BINDING.
DR	InterPro; IPR001438; EGF_II.	FT	DOMAIN	2646	2687	EGF-LIKE 46, CALCIUM-BINDING.
DR	InterPro; IPR006209; EGF-like.	FT	DOMAIN	2688	2727	EGF-LIKE 47, CALCIUM-BINDING.
DR	InterPro; IPR002212; Fibril-assoc.	FT	DOMAIN	115	124	BY SIMILARITY.
DR	Pfam; PF00008; EGF; 44.	FT	DISULFID	125	130	BY SIMILARITY.
DR	Pfam; PF00683; TB; 9.	FT	DISULFID	131	141	BY SIMILARITY.
DR	PRINTS; PR0010; EGFBLD.	FT	DISULFID	142	159	BY SIMILARITY.
DR	SMART; SMO0179; EGF_CA; 43.	FT	DISULFID	160	175	BY SIMILARITY.
DR	PROSITE; PS00010; ASX HYDROXYL; 43.	FT	DISULFID	176	190	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 2.	FT	DISULFID	191	196	BY SIMILARITY.
DR	PROSITE; PS01186; EGF_2; 36.	FT	DISULFID	197	207	BY SIMILARITY.
DR	PROSITE; PS50026; EGF_3; 45.	FT	DISULFID	208	292	BY SIMILARITY.
DR	PROSITE; PS01187; EGF_CA; 43.	FT	DISULFID	293	301	BY SIMILARITY.
KW	Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;	FT	DISULFID	302	316	BY SIMILARITY.
KW	Repeat; Signal; Multigene family.	FT	DISULFID	317	334	BY SIMILARITY.
FT	SIGNAL 1 28 POTENTIAL.	FT	DISULFID	335	343	BY SIMILARITY.
FT	CHAIN 29 2907 FIBRILLIN 2.	FT	DISULFID	344	358	BY SIMILARITY.
FT	DOMAIN 111 142 EGF-LIKE 1.	FT	DISULFID	359	503	BY SIMILARITY.
FT	DOMAIN 145 176 EGF-LIKE 2.	FT	DISULFID	504	512	BY SIMILARITY.
FT	DOMAIN 176 208 EGF-LIKE 3.	FT	DISULFID	513	526	BY SIMILARITY.
FT	DOMAIN 276 317 EGF-LIKE 4.	FT	DISULFID	527	542	BY SIMILARITY.
FT	DOMAIN 318 359 EGF-LIKE 5.	FT	DISULFID	543	551	BY SIMILARITY.
FT	REPEAT 360 426 TGFBP 1.	FT	DISULFID	552	566	BY SIMILARITY.
FT	DOMAIN 487 527 EGF-LIKE 6.	FT	DISULFID	567	584	BY SIMILARITY.
FT	DOMAIN 528 567 EGF-LIKE 7.	FT	DISULFID	585	593	BY SIMILARITY.
FT	DOMAIN 568 609 EGF-LIKE 8.	FT	DISULFID	594	608	BY SIMILARITY.
FT	DOMAIN 610 650 EGF-LIKE 9.	FT	DISULFID	609	625	BY SIMILARITY.
FT	DOMAIN 651 691 EGF-LIKE 10.	FT	DISULFID	626	634	BY SIMILARITY.
FT	REPEAT 692 760 TGFBP 2.	FT	DISULFID	635	649	BY SIMILARITY.
FT	DOMAIN 761 802 EGF-LIKE 11.	FT	DISULFID	650	666	BY SIMILARITY.
FT	DOMAIN 803 844 EGF-LIKE 12.	FT	DISULFID	667	675	BY SIMILARITY.
FT	DOMAIN 845 883 EGF-LIKE 13.	FT	DISULFID	676	690	BY SIMILARITY.
FT	DOMAIN 948 989 EGF-LIKE 14.	FT	DISULFID	691	777	BY SIMILARITY.
FT	REPEAT 990 1065 TGFBP 3.	FT	DISULFID	778	786	BY SIMILARITY.
FT		FT	DISULFID	787	801	BY SIMILARITY.
FT		FT	DISULFID	802	819	BY SIMILARITY.
FT		FT	DISULFID	820	828	BY SIMILARITY.
FT		FT	DISULFID	829	843	BY SIMILARITY.

FT	DISULFID	849	859	BY SIMILARITY.	Db	1518	RTGNCCTDID 1527
FT	DISULFID	854	868	BY SIMILARITY.	RESULT 8		
FT	DISULFID	870	883	BY SIMILARITY.	FBN1 BOVIN		
FT	DISULFID	952	964	BY SIMILARITY.	ID FBN1 BOVIN	STANDARD;	PRT; 2871 AA.
FT	DISULFID	959	973	BY SIMILARITY.	AC P98133;		
FT	DISULFID	975	988	BY SIMILARITY.	DT 01-OCT-1996 (Rel. 34, Created)		
FT	DISULFID	1070	1082	BY SIMILARITY.	DT 01-OCT-1996 (Rel. 34, Last sequence update)		
FT	DISULFID	1077	1091	BY SIMILARITY.	DT 28-FEB-2003 (Rel. 41, Last annotation update)		
FT	DISULFID	1093	1106	BY SIMILARITY.	DE Fibrillin 1 precursor (MP340).		
FT	DISULFID	1112	1124	BY SIMILARITY.	GN FBN1.		
FT	DISULFID	1119	1133	BY SIMILARITY.	OS Bos taurus (Bovine).		
FT	DISULFID	1135	1149	BY SIMILARITY.	OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
FT	DISULFID	1155	1167	BY SIMILARITY.	OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
FT	DISULFID	1162	1176	BY SIMILARITY.	OC Bovidae; Bovinae; Bos.		
FT	DISULFID	1178	1191	BY SIMILARITY.	OC NCBI_TaxID=9913;		
FT	DISULFID	1197	1209	BY SIMILARITY.	OK [1]		
FT	DISULFID	1204	1218	BY SIMILARITY.	RN SEQUENCE FROM N.A.		
FT	DISULFID	1220	1233	BY SIMILARITY.	RP TISSUE=Skin;		
FT	DISULFID	1239	1250	BY SIMILARITY.	RC MEDLINE=95137597; PubMed=7835900;		
FT	DISULFID	1246	1259	BY SIMILARITY.	RX Tilstra D.J., Potter K.A., Byers P.H.;		
FT	DISULFID	1261	1274	BY SIMILARITY.	RA "Sequence of the coding region of the bovine fibrillin cDNA and		
FT	DISULFID	1280	1292	BY SIMILARITY.	RT localization to bovine chromosome 10.";		
FT	DISULFID	1287	1301	BY SIMILARITY.	RL Genomics 23:480-485(1994).		
FT	DISULFID	1303	1316	BY SIMILARITY.	[2]		
FT	DISULFID	1322	1334	BY SIMILARITY.	RP PARTIAL SEQUENCE		
FT	DISULFID	1329	1343	BY SIMILARITY.	RX MEDLINE=96132851; PubMed=8557636;		
FT	DISULFID	1345	1358	BY SIMILARITY.	RA Gibson M.A., Hatzinikolas G., Kumaratilake J.S., Sandberg L.B.,		
FT	DISULFID	1364	1377	BY SIMILARITY.	RA Nicholl J.K., Sutherland G.R., Cleary E.G.;		
FT	DISULFID	1371	1386	BY SIMILARITY.	RT "Further characterization of proteins associated with elastic fiber		
FT	DISULFID	1388	1399	BY SIMILARITY.	RT microfibrils including the molecular cloning of MAGP-2 (MP25).";		
FT	DISULFID	1405	1418	BY SIMILARITY.	RT J. Biol. Chem. 271:1096-1103(1996).		
FT	DISULFID	1412	1427	BY SIMILARITY.	RL CC -!- FUNCTION. Structural component of connective tissue microfibrils		
FT	DISULFID	1429	1440	BY SIMILARITY.	CC that binds calcium. Fibrillin-1-containing microfibrils provide		
FT	DISULFID	1446	1458	BY SIMILARITY.	CC long-term force bearing structural support.		
FT	DISULFID	1453	1467	BY SIMILARITY.	CC -!- PTM: Forms intermolecular disulfide bonds either with other		
FT	DISULFID	1469	1482	BY SIMILARITY.	CC fibrillin-1 molecules or with other components of the		
FT	DISULFID	1488	1499	BY SIMILARITY.	CC microfibrils.		
FT	DISULFID	1494	1508	BY SIMILARITY.	CC -!- SIMILARITY: Contains 47 EGF-like domains.		
FT	DISULFID	1510	1523	BY SIMILARITY.	CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.		
FT	DISULFID	1529	1540	BY SIMILARITY.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration		
FT	DISULFID	1535	1549	BY SIMILARITY.	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -		
FT	DISULFID	1551	1564	BY SIMILARITY.	CC the European Bioinformatics Institute. There are no restrictions on its		
FT	DISULFID	1564	1659	BY SIMILARITY.	CC use by non-profit institutions as long as its content is in no way		
FT	DISULFID	1654	1668	BY SIMILARITY.	CC modified and this statement is not removed. Usage by and for commercial		
FT	DISULFID	1670	1683	BY SIMILARITY.	CC entities requires a license agreement (see http://www.isb-sib.ch/announce/		
FT	DISULFID	1689	1701	BY SIMILARITY.	CC or send an email to license@isb-sib.ch).		
QY	Query Match		13.2%;	Score 374; DB 1; Length 2907;	EMBL; L28748; AAA74122.1; ..		
Db	Best Local Similarity		32.9%;	Pred. No. 3.6e-17;	PIR; A55567; A55567.		
QY	Matches 102; Conservative 24; Mismatches 92; Indels 92; Gaps 18;				HSSP; P35555; 1APJ		
Db	226	DCSVENGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSCNCLCEHFCVNPDP--	283		InterPro; IPR000152; Asx hydroxyl_S.		
QY	1238	ECMINNGCDTQCTNSGSEYSCSEGVALMPDGRSCA-----DIDE--CENNPIC	1287		InterPro; IPR001881; EGF_Ca.		
Db	284	-----QFGYSVCMCTGYRLAADHRCEDVDDCILEPSPCP-ORCVNTQGGFCHCYP	335		InterPro; IPR006209; EGF-like.		
QY	1288	DGGQCTNIPGEYRCLCYDGFMAEMDKTCIDVNECDLNPNICMFGECECTKGSFTCHCQL	1347		InterPro; IPR002212; Fibril-assoc.		
Db	336	NYDLVDGE--QVEPVDPC--FRANCEYOCPLN-QTSVLCVCAEGFA-----PIP	380		Pfam; PF00008; EGF; 46.		
QY	1348	GYSVKKGTGTGCTD-VDECEIGHNCDMEHASCNLNVPFSGKSCREGVNGIKCIDLDECA	1406		Pfam; PF00683; TB; 9.		
Db	381	HEPHRCQFCNQTACPADCPNTQAS--CECEGYILDDGFTCTDIDE-----CENG-	430		SMART; SM00179; EGF_Ca; 42.		
QY	1407	NGTHQCSI-----NAQC-VNTPFSYRCACSEGF-TGDFGTCSDVDECAENTNLCENGQ	1457		PROSITE; PS00010; ASX HYDROXYL; 43.		
Db	431	-----GF-----CS-----GVCHNLPGTFFECICGPDLSALA	455		PROSITE; PS00022; EGF_1; 2.		
QY	1458	CLNVPGAYRCEMGFTPASDSRSQDIDCSFNQICVFGTCNNLPFGMFCICDDGYELD	1517		PROSITE; PS01186; EGF_2; 38.		
Db	456	RHIG--TDGD 463			PROSITE; PS00026; EGF_3; 45.		
QY					PROSITE; PS01187; EGF_Ca; 43.		
Db					Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;		
QY					Repeat; Signal; Multigene family.		
Db					SIGNAL 1 27 POTENTIAL.		
QY					CHAIN 28 2871 FIBRILLIN 1.		
Db					DOMAIN 81 112 EGF-LIKE 1.		
QY					DOMAIN 115 146 EGF-LIKE 2.		
Db					DOMAIN 147 178 EGF-LIKE 3.		
QY					DOMAIN 246 287 EGF-LIKE 4. CALCIUM-BINDING.		

FT	DOMAIN	329	EGF-LIKE 5, CALCIUM-BINDING.	FT	DISULFID	541	555	BY SIMILARITY.
FT	REPEAT	330	TGFBP 1.	FT	DISULFID	547	570	BY SIMILARITY.
FT	DOMAIN	392	PRO-RICH.	FT	DISULFID	576	587	BY SIMILARITY.
FT	DOMAIN	449	EGF-LIKE 6.	FT	DISULFID	582	596	BY SIMILARITY.
FT	DOMAIN	489	EGF-LIKE 7, CALCIUM-BINDING.	FT	DISULFID	598	611	BY SIMILARITY.
FT	DOMAIN	529	EGF-LIKE 8, CALCIUM-BINDING.	FT	DISULFID	617	628	BY SIMILARITY.
FT	DOMAIN	571	EGF-LIKE 9, CALCIUM-BINDING.	FT	DISULFID	623	637	BY SIMILARITY.
FT	DOMAIN	572	EGF-LIKE 10, CALCIUM-BINDING.	FT	DISULFID	639	652	BY SIMILARITY.
FT	DOMAIN	613	TGFBP 2.	FT	DISULFID	727	739	BY SIMILARITY.
FT	REPEAT	654	EGF-LIKE 11, CALCIUM-BINDING.	FT	DISULFID	734	748	BY SIMILARITY.
FT	DOMAIN	723	EGF-LIKE 12, CALCIUM-BINDING.	FT	DISULFID	750	763	BY SIMILARITY.
FT	DOMAIN	765	EGF-LIKE 13, CALCIUM-BINDING.	FT	DISULFID	769	781	BY SIMILARITY.
FT	DOMAIN	807	EGF-LIKE 14, CALCIUM-BINDING.	FT	DISULFID	776	790	BY SIMILARITY.
FT	DOMAIN	910	TGFBP 3.	FT	DISULFID	792	805	BY SIMILARITY.
FT	REPEAT	952	EGF-LIKE 15, CALCIUM-BINDING.	FT	DISULFID	811	821	BY SIMILARITY.
FT	DOMAIN	1028	EGF-LIKE 16, CALCIUM-BINDING.	FT	DISULFID	816	830	BY SIMILARITY.
FT	DOMAIN	1070	EGF-LIKE 17, CALCIUM-BINDING.	FT	DISULFID	832	845	BY SIMILARITY.
FT	DOMAIN	1113	EGF-LIKE 18, CALCIUM-BINDING.	FT	DISULFID	914	926	BY SIMILARITY.
FT	DOMAIN	1155	EGF-LIKE 19, CALCIUM-BINDING.	FT	DISULFID	921	935	BY SIMILARITY.
FT	DOMAIN	1197	EGF-LIKE 20, CALCIUM-BINDING.	FT	DISULFID	937	950	BY SIMILARITY.
FT	DOMAIN	1238	EGF-LIKE 21, CALCIUM-BINDING.	FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DOMAIN	1280	EGF-LIKE 22, CALCIUM-BINDING.	FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DOMAIN	1322	EGF-LIKE 23, CALCIUM-BINDING.	FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DOMAIN	1363	EGF-LIKE 24, CALCIUM-BINDING.	FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DOMAIN	1404	EGF-LIKE 25, CALCIUM-BINDING.	FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DOMAIN	1446	EGF-LIKE 26, CALCIUM-BINDING.	FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DOMAIN	1487	TGFBP 4.	FT	DISULFID	1117	1129	BY SIMILARITY.
FT	REPEAT	1528	EGF-LIKE 27, CALCIUM-BINDING.	FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DOMAIN	1606	EGF-LIKE 28, CALCIUM-BINDING.	FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DOMAIN	1648	TGFBP 5.	FT	DISULFID	1159	1171	BY SIMILARITY.
FT	REPEAT	1689	EGF-LIKE 29, CALCIUM-BINDING.	FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DOMAIN	1766	EGF-LIKE 30, CALCIUM-BINDING.	FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DOMAIN	1808	EGF-LIKE 31, CALCIUM-BINDING.	FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DOMAIN	1849	EGF-LIKE 32, CALCIUM-BINDING.	FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DOMAIN	1891	EGF-LIKE 33, CALCIUM-BINDING.	FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DOMAIN	1930	EGF-LIKE 34, CALCIUM-BINDING.	FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DOMAIN	1973	EGF-LIKE 35, CALCIUM-BINDING.	FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DOMAIN	2013	TGFBP 6.	FT	DISULFID	1265	1278	BY SIMILARITY.
FT	REPEAT	2055	EGF-LIKE 36, CALCIUM-BINDING.	FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DOMAIN	2127	EGF-LIKE 37, CALCIUM-BINDING.	FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DOMAIN	2166	EGF-LIKE 38, CALCIUM-BINDING.	FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DOMAIN	2206	EGF-LIKE 39, CALCIUM-BINDING.	FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DOMAIN	2247	EGF-LIKE 40, CALCIUM-BINDING.	FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DOMAIN	2291	TGFBP 7.	FT	DISULFID	1350	1361	BY SIMILARITY.
FT	REPEAT	2333	EGF-LIKE 41, CALCIUM-BINDING.	FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DOMAIN	2402	EGF-LIKE 42, CALCIUM-BINDING.	FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DOMAIN	2444	EGF-LIKE 43, CALCIUM-BINDING.	FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DOMAIN	2485	EGF-LIKE 44, CALCIUM-BINDING.	FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DOMAIN	2524	EGF-LIKE 45, CALCIUM-BINDING.	FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DOMAIN	2567	EGF-LIKE 46, CALCIUM-BINDING.	FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DOMAIN	2607	EGF-LIKE 47, CALCIUM-BINDING.	FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DOMAIN	2648	BY SIMILARITY.	FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	85	BY SIMILARITY.	FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	89	BY SIMILARITY.	FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	102	BY SIMILARITY.	FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	119	BY SIMILARITY.	FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	123	BY SIMILARITY.	FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	136	BY SIMILARITY.	FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	150	BY SIMILARITY.	FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	154	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	168	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	177	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	250	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	257	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	271	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	273	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	286	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	292	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	299	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	313	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	315	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	328	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	453	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	460	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	474	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	488	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	494	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	499	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	513	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	515	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	528	BY SIMILARITY.	FT	DISULFID			
FT	DISULFID	534	BY SIMILARITY.	FT	DISULFID			

Query Match 13.0%; Score 368; DB 1; Length 2871;
Best Local Similarity 31.5%; Pred. No. 9e-17;
Matches 111, Conservative 26, Mismatches 109; Indels 106; Gaps 20;

Qy	226	DCSVNGGCEHACNAIFGAPRCQCPAGALQADGRSCATATQSCNDLCEHFCVNP----	282
Db	1200	ECSIMNGGCTFTCTNSEGSEVSCQPGFALPMDQRSC-----DIDE--CEDNPNIC	1249
Qy	283	-----DQPGSYSCMCTGYRLADQHRCDVDVDCILEPSPC-PORCVNTGGSECHCYP	335
Db	1250	DGGQCTNIPGEYRCLCYDGFNASDMMKTCVDVNECDLNPICLSGTCENTKGSFICHD	1309
Qy	336	NYDLVDGE--CVEPVDPC--FRANCEYQCOPLNOT-SYLCVCARGFA-----PIP	380

Db 1310 GYSGKKGKGTCTD-INCEIGAHNCBHVACTWAGSKCSPGHWIGDKICTDLDECS 1368
QY 381 HEPHRCOMFCNACPADCPNTOAS--CECPGYILDGFICTDIDEC-EN-----429
Db 1369 NGTHMCSQH-----ADC-KNTMGSVRLCKEGY-TGDGFTCTDLDECSNLCGNGQ 1419
QY 430 -----CGF-----CS-----GVCHNLGTFECICGPPSALA 455
Db 1420 CLNAPGGYRCEDMGFVPSADGKACBIDECSLPNCVFTCHNLGTFECBCEIGYELD 1479
QY 456 RHIG-----TDCDSGK-VDGDSGSGBPSPPTGSLTTPPAVGLV 495
Db 1480 RSGNCTDVNECLDPTTCISGNCVNTPGSYTCDPPD-----FELNPRVGCV 1527
RESULT 9
FBL2 HUMAN STANDARD; PRT; 1184 AA.
AC P98055; AC
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DB Fubulin-2 precursor.
GN FBLN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fibroblast;
RX MEDLINE=95104855; PubMed=7806230;
RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,
Chen M.-L.;
RT "Fubulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
of the gene on human and mouse chromosomes.";
RL Genomics 22:425-430(1994).
[2]
RN DEVELOPMENTAL STAGE.
RP MEDLINE=96301678; PubMed=8737292;
RX Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
early human embryo.";
RL Histochem. J. 28:109-116(1996).
CC -!- FUNCTION: Its binding to fibronectin and some other ligands is
calcium dependent.
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
connective tissues. Expressed in heart, placenta and ovary.
CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
development. Primarily detected within the neuroepithelium, spinal
ganglia and peripheral nerves.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 11 EGF-like domains.
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or send an email to license@ebi-sib.ch).
CC -----
DR EMBL; X82494; CAA57876.1; -.
DR PIR; A55184; A55184.
DR HSSP; P00736; IAPQ.
DR Genew; HGNC:3601; FBLN2.
DR MIM; 135821; -.
GO; GO:0005578; C:extracellular matrix; TAS.

DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 5.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF CA; 9.
DR PROSITE; PS01177; ANAPHYLATOXIN 1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN 2; 3.
DR PROSITE; PS00010; ASX HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF CA; 9.
KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
KW Calcium-binding; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 1184 FIBULIN-2.
FT DOMAIN 28 444 N.
FT DOMAIN 28 177 SUBDOMAIN NB (CYS-FREE).
FT DOMAIN 178 444 SUBDOMAIN NA (CYS-RICH).
FT DOMAIN 445 480 ANAPHYLATOXIN-LIKE 1.
FT DOMAIN 488 519 ANAPHYLATOXIN-LIKE 2.
FT DOMAIN 521 553 ANAPHYLATOXIN-LIKE 3.
FT DOMAIN 604 645 EGF-LIKE 1, CALCIUM-BINDING.
FT DOMAIN 679 718 EGF-LIKE 2.
FT DOMAIN 719 763 EGF-LIKE 3, CALCIUM-BINDING.
FT DOMAIN 764 809 EGF-LIKE 4, CALCIUM-BINDING.
FT DOMAIN 810 857 EGF-LIKE 5, CALCIUM-BINDING.
FT DOMAIN 858 900 EGF-LIKE 6, CALCIUM-BINDING.
FT DOMAIN 901 942 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 943 981 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 982 1024 EGF-LIKE 9, CALCIUM-BINDING.
FT DOMAIN 1025 1069 EGF-LIKE 10, CALCIUM-BINDING.
FT DOMAIN 1070 1184 DOMAIN III.
FT DISULFID 445 472 BY SIMILARITY.
FT DISULFID 446 479 BY SIMILARITY.
FT DISULFID 459 480 BY SIMILARITY.
FT DISULFID 489 518 BY SIMILARITY.
FT DISULFID 502 519 BY SIMILARITY.
FT DISULFID 521 545 BY SIMILARITY.
FT DISULFID 522 552 BY SIMILARITY.
FT DISULFID 535 553 BY SIMILARITY.
FT DISULFID 608 620 BY SIMILARITY.
FT DISULFID 616 629 BY SIMILARITY.
FT DISULFID 631 644 BY SIMILARITY.
FT DISULFID 683 693 BY SIMILARITY.
FT DISULFID 689 702 BY SIMILARITY.
FT DISULFID 704 717 BY SIMILARITY.
FT DISULFID 723 736 BY SIMILARITY.
FT DISULFID 730 745 BY SIMILARITY.
FT DISULFID 751 762 BY SIMILARITY.
FT DISULFID 768 781 BY SIMILARITY.
FT DISULFID 775 790 BY SIMILARITY.
FT DISULFID 796 808 BY SIMILARITY.
FT DISULFID 814 827 BY SIMILARITY.
FT DISULFID 821 836 BY SIMILARITY.
FT DISULFID 843 856 BY SIMILARITY.
FT DISULFID 862 875 BY SIMILARITY.
FT DISULFID 869 884 BY SIMILARITY.
FT DISULFID 886 899 BY SIMILARITY.
FT DISULFID 905 917 BY SIMILARITY.
FT DISULFID 913 926 BY SIMILARITY.
FT DISULFID 928 941 BY SIMILARITY.
FT DISULFID 947 956 BY SIMILARITY.
FT DISULFID 952 965 BY SIMILARITY.
FT DISULFID 967 980 BY SIMILARITY.
FT DISULFID 986 998 BY SIMILARITY.
FT DISULFID 994 1007 BY SIMILARITY.
FT DISULFID 1009 1023 BY SIMILARITY.

FT DISULFID 1029 1042 BY SIMILARITY.
 FT DISULFID 1036 1051 BY SIMILARITY.
 FT DISULFID 1056 1068 BY SIMILARITY.
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1035 1035 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1184 AA; 126543 MW; CA48490A55F9ECSD CRC64;
 Query Match 13.0%; Score 367.5; DB 1; Length 1184;
 Best Local Similarity 30.0%; Pred. No. 4.1e-17;
 Matches 119; Conservative 29; Mismatches 124; Indels 125; Gaps 21;
 QY 136 EEOQCEVKAD-GFLCEFHPRATC-----RPLAV-----EPGAAAAAASITGTTPFAARG 183
 Db 531 EGQSCSNFNLGPPCN-HVMSLSCBEEPLIVEVRPPEPAAPRRVS-----EAEH 582
 QY 184 ADFOALPVGSSAAV---APLGLQIMCTAPPGAVQGHWAREAPGAWDCSVENGCGCEHACNA 240
 Db 583 AGREALSLGTEAELPNSLPDGDQDECLLPGL-----CQHLCLIN 622
 QY 241 IPGAPRCQCPAGAAQADGRSC-----TASAT-----QS 269
 Db 623 TVGSYHCACPGFSLQDDGRTCPGHPPOPEAPQEPALKSEFSQVASTPIPLPQNPNT 652
 QY 270 CND--LCEHFCVNPDPQSGYSQWCTGYRLAADOHRCEVDVDCILEPSPCP--QRQCVNT 325
 Db 683 CKDNGPKQVC--STVGGSAISCSPGYAIMADGVSCEDINECVDTLHTCSRGEHCVNT 739
 QY 326 QGGEFECH---CYPNYDLVDGCEVPVDPFRANCEYQCOPLNQTSLVLCV----- 371
 Db 740 LGSFHCYKALTCBPGYALKDGECE-EDVDEC--AMGHTCQF-----GFLCQNTKGSFYCQA 792
 QY 372 ---CARGFAIPH-----EPHRCQMFQNTACPADCDNTQASCPCPGY-I 414
 Db 793 RQRCMDGFLQDPBGNVDINECTSLSPFCRPGSCINTVGSYTCORNPLI---CARGYHA 849
 QY 415 LDGDFICTDIDECENGFCSCG---VCHNLPGTPECIC 448
 Db 850 SDDGAKVDVNBETGVHRCGEQVCHNLPGSYRCDC 886
 RESULT 10
 FBNI_PIG
 ID FBNI_PIG STANDARD; PRT; 2871 AA.
 AC QSTV36;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Fibrillin 1 precursor.
 GN FBNI.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=99156858; PubMed=10036187;
 RA Biery N.J.; Eldadah Z.A.; Moore C.S.; Stetten G.; Spencer F.,
 RA Dietz H.C.;
 RT "Revised genomic organization of FBNI and significance for regulated
 RT gene expression."
 RL Genomics 56:70-77(1999).
 CC -!- FUNCTION: Structural component of connective tissue microfibrils
 CC that binds calcium. Fibrillin-1-containing microfibrils provide
 CC long-term force bearing structural support.
 CC -!- PFM: Forms intermolecular disulfide bonds either with other
 CC fibrillin-1 molecules or with other components of the
 CC microfibrils.
 CC -!- SIMILARITY: Contains 47 EGF-like domains.
 CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF073800; RAD50328.1; --
 DR HSSP; P35555; IAPU.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00008; EGF; 44.
 DR Pfam; PF00883; TB; 9.
 DR SMART; SM00179; EGF_CA; 40.
 DR PROSITE; PS00010; ASX_HYDROXYL; 41.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 36.
 DR PROSITE; PS50026; EGF_3; 43.
 DR PROSITE; PS01187; EGF_CA; 41.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 2871 FIBRILLIN 1.
 FT DOMAIN 81 112 EGF-LIKE 1.
 FT DOMAIN 115 146 EGF-LIKE 2.
 FT DOMAIN 147 178 EGF-LIKE 3.
 FT DOMAIN 246 287 EGF-LIKE 4. CALCIUM-BINDING.
 FT DOMAIN 288 329 EGF-LIKE 5. CALCIUM-BINDING.
 FT REPEAT 330 390 TGFBP 1.
 FT DOMAIN 392 446 PRO-RICH.
 FT DOMAIN 449 489 EGF-LIKE 6.
 FT DOMAIN 490 529 EGF-LIKE 7. CALCIUM-BINDING.
 FT DOMAIN 530 571 EGF-LIKE 8. CALCIUM-BINDING.
 FT DOMAIN 572 612 EGF-LIKE 9. CALCIUM-BINDING.
 FT DOMAIN 613 653 EGF-LIKE 10. CALCIUM-BINDING.
 FT REPEAT 654 722 TGFBP 2.
 FT DOMAIN 723 764 EGF-LIKE 11. CALCIUM-BINDING.
 FT DOMAIN 765 806 EGF-LIKE 12. CALCIUM-BINDING.
 FT DOMAIN 807 846 EGF-LIKE 13. CALCIUM-BINDING.
 FT DOMAIN 910 951 EGF-LIKE 14. CALCIUM-BINDING.
 FT REPEAT 952 1027 TGFBP 3.
 FT DOMAIN 1028 1069 EGF-LIKE 15. CALCIUM-BINDING.
 FT DOMAIN 1070 1112 EGF-LIKE 16. CALCIUM-BINDING.
 FT DOMAIN 1113 1154 EGF-LIKE 17. CALCIUM-BINDING.
 FT DOMAIN 1155 1196 EGF-LIKE 18. CALCIUM-BINDING.
 FT DOMAIN 1197 1237 EGF-LIKE 19. CALCIUM-BINDING.
 FT DOMAIN 1238 1279 EGF-LIKE 20. CALCIUM-BINDING.
 FT DOMAIN 1280 1321 EGF-LIKE 21. CALCIUM-BINDING.
 FT DOMAIN 1322 1362 EGF-LIKE 22. CALCIUM-BINDING.
 FT DOMAIN 1363 1403 EGF-LIKE 23. CALCIUM-BINDING.
 FT DOMAIN 1404 1445 EGF-LIKE 24. CALCIUM-BINDING.
 FT DOMAIN 1446 1486 EGF-LIKE 25. CALCIUM-BINDING.
 FT DOMAIN 1487 1527 EGF-LIKE 26. CALCIUM-BINDING.
 FT REPEAT 1528 1605 TGFBP 4.
 FT DOMAIN 1606 1647 EGF-LIKE 27. CALCIUM-BINDING.
 FT DOMAIN 1648 1688 EGF-LIKE 28. CALCIUM-BINDING.
 FT REPEAT 1689 1765 TGFBP 5.
 FT DOMAIN 1766 1807 EGF-LIKE 29. CALCIUM-BINDING.
 FT DOMAIN 1808 1848 EGF-LIKE 30. CALCIUM-BINDING.
 FT DOMAIN 1849 1890 EGF-LIKE 31. CALCIUM-BINDING.
 FT DOMAIN 1891 1929 EGF-LIKE 32. CALCIUM-BINDING.
 FT DOMAIN 1930 1972 EGF-LIKE 33. CALCIUM-BINDING.
 FT DOMAIN 1973 2012 EGF-LIKE 34. CALCIUM-BINDING.
 FT DOMAIN 2013 2054 EGF-LIKE 35. CALCIUM-BINDING.
 FT REPEAT 2055 2126 TGFBP 6.
 FT DOMAIN 2127 2165 EGF-LIKE 36. CALCIUM-BINDING.
 FT DOMAIN 2166 2205 EGF-LIKE 37. CALCIUM-BINDING.
 FT DOMAIN 2206 2246 EGF-LIKE 38. CALCIUM-BINDING.
 FT DOMAIN 2247 2290 EGF-LIKE 39. CALCIUM-BINDING.
 FT DOMAIN 2291 2332 EGF-LIKE 40. CALCIUM-BINDING.
 FT REPEAT 2333 2401 TGFBP 7.

RT component preferentially located in elastic matrices.";
 RL J. Cell Biol. 124:855-863 (1994).
 RN [2]
 RP SEQUENCE OF 752-1505 FROM N.A.
 RX MEDLINE=91304567; PubMed=1852206;
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
 RA Tsipouras P., Ramirez F., Hollister D.;
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to
 RT two different fibrillin genes.";
 RL Nature 352:330-334 (1991).
 RN [3]
 RP VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.
 RX MEDLINE=96083599; PubMed=7493032;
 RA Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;
 RT "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,
 RT congenital contractural arachnodactyly.";
 RL Nat. Genet. 11:456-458 (1995).
 RN [4]
 RP VARIANT CCA HIS-1114.
 RX MEDLINE=98407789; PubMed=9737771;
 RA Babcock D., Gaerner C., Francke U., Maalen C.;
 RT "A single mutation that results in an app-to-his substitution and
 RT partial exon skipping in a family with congenital contractural
 RT arachnodactyly.";
 RL Hum. Genet. 103:22-28 (1998).
 RN [5]
 RP VARIANTS CCA PHE-1141 AND TRP-1252.
 RX MEDLINE=20259236; PubMed=10797416;
 RA Belleh S., Zhou G., Wang M., Der Kaloustian V.M., Pagon R.A.,
 RA Godfrey M.;
 RT "Two novel fibrillin-2 mutations in congenital contractural
 RT arachnodactyly.";
 RL Am. J. Med. Genet. 92:7-12 (2000).
 CC -!- FUNCTION: Structural component of connective tissue microfibrils
 CC that binds calcium. Fibrillin-2-containing microfibrils regulate
 CC the early process of elastic fiber assembly.
 CC -!- DISEASE: Defects in FBN2 are the cause of congenital contractural
 CC arachnodactyly (CCA) [MIM:121050]; also known as Beals syndrome.
 CC CCA is phenotypically similar to Marfan syndrome, but does not
 CC effect the aorta and the eyes.
 CC -!- SIMILARITY: Contains 47 EGF-like domains.
 CC -!- DATABASE: Contains 7 TGF-beta binding protein (TGFBP) domains.
 CC -!- DATABASE: NAME=Elastic Fiber Homepage; NOTE=Fibrillin 2 page;
 CC WWW="http://ef.wustl.edu/genes/FBN2.htm".
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 CC -----
 CC EMBL: U03272; AAA18950.1; -;
 CC EMBL: X62009; -; NOT_ANNOTATED_CDS.
 CC PIR: A54105; A54105.
 CC HSSP: P35555; 1EMN.
 CC Genew: HGNC:3604; FBN2.
 CC MIM: 121050; -;
 CC GO: GO:0005578; C:extracellular matrix; TAS.
 CC GO: GO:0005201; P:extracellular matrix structural constituent; TAS.
 CC GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.
 CC GO: GO:0007397; P:histogenesis and organogenesis; TAS.
 CC InterPro: IPR00152; Asx hydroxyl_s.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR001438; EGF_I1.
 CC InterPro: IPR006209; EGF_Like.
 CC InterPro: IPR002212; Fibril-assoc.
 CC Pfam: PF00008; EGF; 45.
 CC PRINTS: PR00010; EGFBL00D.
 CC SMART: SM00179; EGF_CA; 43.
 CC PROSITE: PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 37.
 DR PROSITE; PS00026; EGF_3; 45.
 DR PROSITE; PS01187; EGF_CA; 42.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.
 FT SIGNAL 1 28
 FT CHAIN 29 2911
 FT DOMAIN 111 142
 FT DOMAIN 145 176
 FT DOMAIN 176 207
 FT DOMAIN 275 316
 FT DOMAIN 317 358
 FT REPEAT 359 425
 FT DOMAIN 493 533
 FT DOMAIN 534 573
 FT DOMAIN 574 615
 FT DOMAIN 616 656
 FT DOMAIN 657 697
 FT REPEAT 766 766
 FT DOMAIN 767 808
 FT DOMAIN 809 850
 FT DOMAIN 851 890
 FT DOMAIN 954 995
 FT REPEAT 996 1071
 FT DOMAIN 1072 1113
 FT DOMAIN 1114 1156
 FT DOMAIN 1157 1198
 FT DOMAIN 1199 1240
 FT DOMAIN 1241 1281
 FT DOMAIN 1282 1323
 FT DOMAIN 1324 1365
 FT DOMAIN 1366 1406
 FT DOMAIN 1407 1447
 FT DOMAIN 1448 1489
 FT DOMAIN 1490 1530
 FT DOMAIN 1531 1571
 FT REPEAT 1572 1648
 FT DOMAIN 1649 1690
 FT DOMAIN 1691 1732
 FT REPEAT 1733 1806
 FT DOMAIN 1807 1848
 FT DOMAIN 1849 1890
 FT DOMAIN 1891 1932
 FT DOMAIN 1933 1971
 FT DOMAIN 1972 2014
 FT DOMAIN 2015 2054
 FT DOMAIN 2055 2096
 FT REPEAT 2097 2169
 FT DOMAIN 2170 2211
 FT DOMAIN 2212 2251
 FT DOMAIN 2252 2292
 FT DOMAIN 2293 2336
 FT DOMAIN 2337 2378
 FT REPEAT 2379 2447
 FT DOMAIN 2448 2489
 FT DOMAIN 2490 2530
 FT DOMAIN 2531 2569
 FT DOMAIN 2570 2612
 FT DOMAIN 2613 2652
 FT DOMAIN 2653 2693
 FT DOMAIN 2694 2733
 FT DISULFID 115 124
 FT DISULFID 119 130
 FT DISULFID 132 141
 FT DISULFID 149 159
 FT DISULFID 153 164
 FT DISULFID 166 175
 FT DISULFID 180 190
 FT DISULFID 184 195
 FT DISULFID 197 206
 FT DISULFID 199 291
 FT DISULFID 286 300

10-OCT-2003 (Rel. 42, Last annotation update)

DT DE FBNI OR FBN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RP MEDLINE=93372860; PubMed=8364578;
RX Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
RA Panglilian T., Bonadio J.;
RA "Genomic organization of the sequence coding for fibrillin, the
RT defective gene product in Marfan syndrome.";
RT Hum. Mol. Genet. 2:961-968(1993).
RN [2]
RN
RN SEQUENCE OF 1-932 FROM N.A.
RP TISSUE=Fibroblast, and Placenta;
RX MEDLINE=94010947; PubMed=7691719;
RA Corson G.M., Chabberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
RA "Fibrillin binds calcium and is coded by cDNAs that reveal a
RT multidomain structure and alternatively spliced exons at the 5'
RT end.";
RT Genomics 17:476-484(1993).
RN [3]
RN
RN SEQUENCE OF 899-2871 FROM N.A.
RX MEDLINE=91304568; PubMed=1852207;
RA Maslin C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
RT "Partial sequence of a candidate gene for the Marfan syndrome.";
RN [4]
RN
RN SEQUENCE OF 813-1313 FROM N.A.
RX MEDLINE=91304567; PubMed=1852206;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras F., Ramirez F., Hollister D.W.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RN [5]
RN
RN CHARACTERIZATION.
RX MEDLINE=91317849; PubMed=1860873;
RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;
RT "Purification and partial characterization of fibrillin, a cysteine-
RT rich structural component of connective tissue microfibrils.";
RN [6]
RN
RN STRUCTURE BY NMR OF 2054-2125.
RX MEDLINE=98031893; PubMed=9362480;
RA Yuan X., Downing A.K., Knott V., Handford P.A.;
RT "Solution structure of the transforming growth factor beta-binding
RT protein-like module, a domain associated with matrix fibrils.";
RN [7]
RN
RN STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96144829; PubMed=8568869;
RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
RT "Calcium binding properties of an epidermal growth factor-like domain
RT pair from human fibrillin-1";
RN [8]
RN
RN STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96222301; PubMed=8653794;
RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
RA Handford P.A.;
RT "Solution structure of a pair of calcium-binding epidermal growth
RT factor-like domains: implications for the Marfan syndrome and other
RT genetic disorders.";
RN [9]
RN
RN REVIEW ON MFS VARIANTS.
RX MEDLINE=96174615; PubMed=8594563;
RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;

factor-like domains: implications for the Marfan syndrome and other genetic disorders.";
Cell 85:597-605(1996).
[9]
REVIEW ON MFS VARIANTS.
MEDLINE=96174615; PubMed=8594563;
Colled G., Beroud C., Soussi T., Junien C., Boileau C.;

178	EGF-LIKE 3.	CALCIUM-BINDING.
287	EGF-LIKE 4.	CALCIUM-BINDING.
329	EGF-LIKE 5.	CALCIUM-BINDING.
401	TGFBP 1.	
446	PRO-RICH.	
489	EGF-LIKE 6.	
529	EGF-LIKE 7.	CALCIUM-BINDING.
571	EGF-LIKE 8.	CALCIUM-BINDING.
612	EGF-LIKE 9.	CALCIUM-BINDING.
653	EGF-LIKE 10.	CALCIUM-BINDING.
721	TGFBP 2.	
764	EGF-LIKE 11.	CALCIUM-BINDING.
806	EGF-LIKE 12.	CALCIUM-BINDING.
846	EGF-LIKE 13.	CALCIUM-BINDING.
951	EGF-LIKE 14.	CALCIUM-BINDING.
1018	TGFBP 3.	
1069	EGF-LIKE 15.	CALCIUM-BINDING.
1111	EGF-LIKE 16.	CALCIUM-BINDING.
1154	EGF-LIKE 17.	CALCIUM-BINDING.
1196	EGF-LIKE 18.	CALCIUM-BINDING.
1237	EGF-LIKE 19.	CALCIUM-BINDING.
1279	EGF-LIKE 20.	CALCIUM-BINDING.
1321	EGF-LIKE 21.	CALCIUM-BINDING.
1362	EGF-LIKE 22.	CALCIUM-BINDING.
1403	EGF-LIKE 23.	CALCIUM-BINDING.
1445	EGF-LIKE 24.	CALCIUM-BINDING.
1486	EGF-LIKE 25.	CALCIUM-BINDING.
1527	EGF-LIKE 26.	CALCIUM-BINDING.
1559	TGFBP 4.	
1647	EGF-LIKE 27.	CALCIUM-BINDING.
1688	EGF-LIKE 28.	CALCIUM-BINDING.
1758	TGFBP 5.	
1807	EGF-LIKE 29.	CALCIUM-BINDING.
1848	EGF-LIKE 30.	CALCIUM-BINDING.
1890	EGF-LIKE 31.	CALCIUM-BINDING.
1929	EGF-LIKE 32.	CALCIUM-BINDING.
1972	EGF-LIKE 33.	CALCIUM-BINDING.
2012	EGF-LIKE 34.	CALCIUM-BINDING.
2054	EGF-LIKE 35.	CALCIUM-BINDING.
2121	TGFBP 6.	
2165	EGF-LIKE 36.	CALCIUM-BINDING.
2205	EGF-LIKE 37.	CALCIUM-BINDING.
2246	EGF-LIKE 38.	CALCIUM-BINDING.
2289	EGF-LIKE 39.	CALCIUM-BINDING.
2332	EGF-LIKE 40.	CALCIUM-BINDING.
2400	TGFBP 7.	
2443	EGF-LIKE 41.	CALCIUM-BINDING.
2484	EGF-LIKE 42.	CALCIUM-BINDING.
2523	EGF-LIKE 43.	CALCIUM-BINDING.
2566	EGF-LIKE 44.	CALCIUM-BINDING.
2606	EGF-LIKE 45.	CALCIUM-BINDING.
2647	EGF-LIKE 46.	CALCIUM-BINDING.
2687	EGF-LIKE 47.	CALCIUM-BINDING.
94	BY SIMILARITY.	
100	BY SIMILARITY.	
111	BY SIMILARITY.	
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134	BY SIMILARITY.	
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465	BY SIMILARITY.	
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488	BY SIMILARITY.	
504	BY SIMILARITY.	
513	BY SIMILARITY.	

FT DISULFID 515 BY SIMILARITY.
FT DISULFID 534 BY SIMILARITY.
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FT DISULFID 1450 BY SIMILARITY.
FT DISULFID 1456 BY SIMILARITY.
FT DISULFID 1472 BY SIMILARITY.
FT DISULFID 1485 BY SIMILARITY.
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FT DISULFID 1497 BY SIMILARITY.
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FT DISULFID 1610 BY SIMILARITY.
FT DISULFID 1617 BY SIMILARITY.
FT DISULFID 1631 BY SIMILARITY.
FT DISULFID 1633 BY SIMILARITY.
FT DISULFID 1646 BY SIMILARITY.
FT DISULFID 1652 BY SIMILARITY.
FT DISULFID 1658 BY SIMILARITY.
FT DISULFID 1672 BY SIMILARITY.
Query Match 12.8%; Score 362; DB 1; Length 2871;
Best Local Similarity 29.4%; Pred. No. 2.e-15;
Matches 117; Conservative 26; Mismatches 127; Indels 128; Gaps 21;
194 SAIVAPIGL-----QLMCTAPPAGVGHWAREAPGAWDCSVNGGCEHACNAIPGAPRC 247
1162 SANLCPHGRGVNLIGKYQCACNPGYHPTDRLFCVDIDECISINNGGCTETCTNSDGSYEC 1221
248 QCPAGALQADGRSCTASATQSCNDLCEHFCVNP-----DQPGSYSCMCTGYRL 298

Db 1222 SCQGFALMPDQSRCT-----DIDQ--CENPNICDGGQCTNIEGTRCLCYDGFMA 1271
Qy 299 AADQHRCEVDCCILBSPC-PQRCVNTQGGFCHCYPNYDLVDGE--CVEPVDPC--FR 353
Db 1272 SEMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSKKGTGCTD-INECEIGA 1330
Qy 354 ANCEYQCOPLNQF-SYLCVCAEFGA-----PIPEPHRCQMCNQTACDADCPN 402
Db 1331 HNCGRHAVCTNTAGSKFCSCPGWIGDKICTDLBCSNGTHMCSQH-----ADC-KN 1382
Qy 403 TOAS--CECEGYILDGFICTIDEC-EN-----GGF----- 432
Db 1383 TMGSYRCLCKDGY-TGDGFTCTDLDECSENILNCGNQCCLNAPGGYRCCECDMGFVPSADG 1441
Qy 433 -----CS-----GVCHNLPGTFECICGPDPSALARHIG-----TDCDSGK 466
Db 1442 KACEDIDECSLPNICVFGTCHNLPGLFRCEIGEYELDRSGNCTDWNELDPTTCISGN 1501
Qy 467 VOGDSSGSGEPSPPTGS-----TLTPPAVGLV 495
Db 1502 CVN-----TPGSYTCDCSPDFELNPTRVGCV 1527
RESULT 14
FBL2 MOUSE
ID FBL2 MOUSE STANDARD; PRT; 1221 AA.
AC P3789; Q9WU12;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibulin-2 precursor.
GN FBLN2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=8245130;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding".
RL J. Cell Biol. 123:1269-1277(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization".
RL Eur. J. Biochem. 263:471-477(1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=97003230; PubMed=8850569;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo".
RL Dev. Dyn. 205:348-364(1996).
RN [4]
RP BINDING TO LAMA2.
RX MEDLINE=99146904; PubMed=10022829;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
RT extracellular matrix proteins".
RL EMBO J. 18:863-870(1999).
RN [5]
RP DOWN-REGULATION BY GLUCOCORTICOIDS.
RX MEDLINE=21600963; PubMed=11737251;
RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
RT "Glucocorticoids down-regulate the extracellular matrix proteins

fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 Eur. J. Haematol. 67:176-184(2001)).
 CC -!- FUNCTION: Its binding to fibronectin and some other ligands is
 CC calcium dependent.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P37889-1; Sequence=Displayed;
 CC Name=2; Synonyms=EGF3-less;
 CC IsoId=P37889-2; Sequence=VSP_001391;
 CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
 CC connective tissues.
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
 CC family contributes to the formation of molecularly distinct
 CC extracellular matrices already during early developmental stages
 CC of a large number of tissues.
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 11 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X75285; CAA53040.1; --
 CC EMBL; AF135253; AAD34456.1; --
 CC EMBL; AF135239; AAD34456.1; JOINED.
 CC EMBL; AF135240; AAD34456.1; JOINED.
 CC EMBL; AF135241; AAD34456.1; JOINED.
 CC EMBL; AF135242; AAD34456.1; JOINED.
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 CC EMBL; AF135246; AAD34456.1; JOINED.
 CC EMBL; AF135247; AAD34456.1; JOINED.
 CC EMBL; AF135248; AAD34456.1; JOINED.
 CC EMBL; AF135249; AAD34456.1; JOINED.
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 CC EMBL; AF135252; AAD34456.1; JOINED.
 CC EMBL; AF135253; AAD34456.1; JOINED.
 CC PIR; A49457; A49457.
 CC HSP; P00736; IAPQ.
 CC MGD; MGI:95488; Fbln2.
 CC InterPro; IPR000020; Anaphylatoxin.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR006209; EGF_like.
 CC Pfam; PF01821; ANATO; 2.
 CC Pfam; PF00008; EGF; 5.
 CC SMART; SM00104; ANATO; 3.
 CC SMART; SM00179; EGF_CA; 9.
 CC PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 CC PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 CC PROSITE; PS00010; ASX_HYDROXYL; 5.
 CC PROSITE; PS00022; EGF_1; FALSE_NEG.
 CC PROSITE; PS0186; EGF_2; 5.
 CC PROSITE; PS00026; EGF_3; 5.
 CC PROSITE; PS0187; EGF_CA; 10.
 CC Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 CC Calcium-binding; Alternative splicing; Repeat.
 CC SIGNAL 1 26
 CC CHAIN 27 1221 FIBULIN-2.
 CC DOMAIN 27 434 N.
 CC DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).

FT	DOMAIN	177	434	SUBDOMAIN NB (CYS-FREE).
FT	DOMAIN	435	477	ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	478	510	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	511	543	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	594	635	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	669	708	EGF-LIKE 2.
FT	DOMAIN	709	755	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	756	800	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	801	846	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	847	894	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	895	937	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	938	979	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	980	1018	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1019	1061	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1062	1106	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1111	1221	DOMAIN III.
FT	SITE	421	423	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	435	462	BY SIMILARITY.
FT	DISULFID	436	469	BY SIMILARITY.
FT	DISULFID	449	508	BY SIMILARITY.
FT	DISULFID	492	509	BY SIMILARITY.
FT	DISULFID	511	535	BY SIMILARITY.
FT	DISULFID	512	542	BY SIMILARITY.
FT	DISULFID	525	543	BY SIMILARITY.
FT	DISULFID	598	610	BY SIMILARITY.
FT	DISULFID	606	619	BY SIMILARITY.
FT	DISULFID	621	634	BY SIMILARITY.
FT	DISULFID	673	683	BY SIMILARITY.
FT	DISULFID	679	692	BY SIMILARITY.
FT	DISULFID	694	707	BY SIMILARITY.
FT	DISULFID	713	726	BY SIMILARITY.
FT	DISULFID	720	735	BY SIMILARITY.
FT	DISULFID	742	754	BY SIMILARITY.
FT	DISULFID	805	818	BY SIMILARITY.
FT	DISULFID	812	827	BY SIMILARITY.
FT	DISULFID	833	845	BY SIMILARITY.
FT	DISULFID	899	912	BY SIMILARITY.
FT	DISULFID	906	921	BY SIMILARITY.
FT	DISULFID	923	936	BY SIMILARITY.
FT	DISULFID	942	954	BY SIMILARITY.
FT	DISULFID	950	963	BY SIMILARITY.
FT	DISULFID	965	978	BY SIMILARITY.
FT	DISULFID	984	993	BY SIMILARITY.
FT	DISULFID	989	1002	BY SIMILARITY.
FT	DISULFID	1004	1017	BY SIMILARITY.
FT	DISULFID	1023	1035	BY SIMILARITY.
FT	DISULFID	1031	1044	BY SIMILARITY.
FT	DISULFID	1046	1060	BY SIMILARITY.
FT	DISULFID	1066	1079	BY SIMILARITY.
FT	DISULFID	1073	1088	BY SIMILARITY.
FT	DISULFID	1093	1105	BY SIMILARITY.
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	497	497	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	737	737	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1072	1072	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	709	755	Missing (in isoform 2).
FT	CONFLICT	140	159	/FTIDEVSP_001391.
FT	CONFLICT	348	348	HSGRKAAGTHTVHLSRCAC -> TVAVSICWYRPPPLILP
FT	CONFLICT	507	507	S -> L (IN REF. 2).
FT	CONFLICT	1102	1102	Q -> QO (IN REF. 2).
FT	CONFLICT	1102	1102	Q -> E (IN REF. 2).
FT	SEQUENCE	1221	1221	AA; 131818 MW; 87DB2A10A8FDC45F CRC64;
FT	SEQUENCE	1221	1221	AA; 131818 MW; 87DB2A10A8FDC45F CRC64;

Query Match 12.6%; Score 357; DB 1; Length 1221;
 Best Local Similarity 29.5%; Pred. No. 2, 1e-16;
 Matches 123; Conservative 39; Mismatches 141; Indels 114; Gaps 27;

QY	136	EQQCEVKAD-GFLCFHFHFPATC-----RPLAV-----EPGAAAAAASV-----IT 174
DB	521	EQQCESNPNLGYPCN-HVMLSCCEGEPLIVPEVRRPPPEAARRVSEMEASREALS 579


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FT NON TER 1 1
SQ SEQUENCE 625 AA; 65876 MW; 3E5E161183A854B9 CRC64;

Query Match 99.9%; Score 2826; DB 4; Length 625;
Best Local Similarity 99.8%; Pred. No. 1.2e-225;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
DB 69 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 128
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPVCV 120
DB 129 GGVGRRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPVCV 188
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPTFA 180
DB 189 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPTFA 248
QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPVAGVQGHWAREAPGAWDCSVENGCCHEACNA 240
DB 249 ARGADFOALPVGSSAAVAPLGLQLMCTAPPVAGVQGHWAREAPGAWDCSVENGCCHEACNA 308
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
DB 309 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 368
QY 301 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDGSCVPEVDPFCFRANCEYQC 360
DB 369 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDGSCVPEVDPFCFRANCEYQC 428
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECEPEGYLLDDGFI 420
DB 429 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECEPEGYLLDDGFI 488
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALHARHIGTDCDSKGVDDSGSGSEPPPS 480
DB 489 CTDIDECENGFCGSGVCHNLPGTFECICGPDALHARHIGTDCDSKGVDDSGSGSEPPPS 548
QY 481 PTFGSLTTPPAVGLVHSG 498
DB 549 PTFGSLTTPPAVGLVHSG 566

RESULT 2
Q9UC32 PRELIMINARY; PRT; 468 AA.
AC Q9UC32;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN RP
RP SEQUENCE.
RX MEDLINE=93293792; PubMed=8390446;
RA Yamamoto S., Mizoguchi T., Tamaki T., Ohkuchi M., Kimura S., Aoki N.;
RT "Urinary thrombomodulin, its isolation and characterization.";
RL J. Biochem. 113:433-440(1993).
HSSP: P07204; 1ZAQ.
DB GO:0016020; C:membrane; IEA.
DB GO:0005509; F:calcium ion binding; IEA.
DB GO:0005529; F:sugar binding; IEA.
DB GO:0004888; F:transmembrane receptor activity; IEA.
DB GO:0007596; P:blood coagulation; IEA.
DB InterPro: IPR000152; ASX hydroxyl S.
DB InterPro: IPR001881; EGF CA.
DB InterPro: IPR006209; EGF like.
DB InterPro: IPR006210; IEGF.
DB InterPro: IPR001304; Lectin_C.

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DR InterPro: IPR001491; Thrombomodulin.
DR Pfam: PF00008; EGF; 3.
DR PRINTS: PR00059; lectin c; 1.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00181; EGF; 6.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS00441; C_TYPE_LLECTIN_2; 1.
DR PROSITE: PS01186; EGF 2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 468 AA; 49444 MW; 4BFE8E98E8B6A40 CRC64;

Query Match 93.9%; Score 2658; DB 4; Length 468;
Best Local Similarity 99.8%; Pred. No. 6.9e-212;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
DB 1 APAEPQGGSCQVEHDCFCALYPGPATFLNASQICDGLRGHLMTVRSSVAADVLSLLNGD 60
QY 61 GGVGRRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPVCV 120
DB 61 GGVGRRRLWIGLQLPFGCGDPKRLGRLGFQWVTGDNNTSYSRWARLDLNGAPLCPVCV 120
QY 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPTFA 180
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYGTPTFA 180
QY 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPVAGVQGHWAREAPGAWDCSVENGCCHEACNA 240
DB 181 ARGADFOALPVGSSAAVAPLGLQLMCTAPPVAGVQGHWAREAPGAWDCSVENGCCHEACNA 240
QY 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
DB 241 IPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPQPGSYSCMCTGYRLAA 300
QY 301 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDGSCVPEVDPFCFRANCEYQC 360
DB 301 DOHRCEDVDDCILEPSPQPCQRCVNTQGGFECHCYPNYDLVDGSCVPEVDPFCFRANCEYQC 360
QY 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECEPEGYLLDDGFI 420
DB 361 QPLNQTSLVCVCAEGFAPIPHEPHRCQMFNCNOTACPADCDPNTQASCECEPEGYLLDDGFI 420
QY 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALHARHIGTDCDSKGVDDSGSGSEPPPS 468
DB 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALHARHIGTDCDSKGVDDSGSGSEPPPS 468

RESULT 3
Q8HZ48 PRELIMINARY; PRT; 580 AA.
AC Q8HZ48;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thrombomodulin precursor.
GN THBD.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN RP
RP SEQUENCE FROM N.A.
RA Deming C.B., Kim A.Y., Rade J.J.;
RT "Cloning of rabbit thrombomodulin cDNA sequence.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY138902; AAN15931.2; -.
DR PIR: A33308; A33308.
DB GO:0016020; C:membrane; IEA.
DB GO:0005509; F:calcium ion binding; IEA.
DB GO:0005529; F:sugar binding; IEA.

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DR GO: 0004888; F:transmembrane receptor activity; IEA.
 DR GO: 0007596; P: blood coagulation; IEA.
 DR InterPro: IPR000152; Asx hydroxyl_S.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR001491; Thrombomodulin.
 DR Pfam: PF00008; EGF.
 DR PRINTS: PR00907; THROMBOMODULN.
 DR SMART: SM00034; CLECT. 1.
 DR SMART: SM00181; EGF. 6.
 DR SMART: SM00179; EGF_Ca. 4.
 DR PROSITE: PS00010; ASX HYDROXYL; 2.
 DR PROSITE: PS00041; C TYPE LECTIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_Ca; 2.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 1 19 POTENTIAL.
 GO 580 AA; 60115 MW; ABA328FD2E141F42 CRC64;
 Query Match 70.2%; Score 1987.5; DB 6; Length 580;
 Best Local Similarity 71.6%; Pred. No. 3e-156;
 Matches 363; Conservative 27; Mismatches 98; Indels 19; Gaps 8;
 QY 3 AEPQPGSQCVHDCFPATFLNASQICDGLRGLMTVRSSVAADVVISLLNGDGG 62
 Db 23 AEPQPGSQCVHDCFPATFLNASQICDGLRGLMTVRSSVAADVVISLLNGDGG 81
 QY 63 VGRRLWIGLQPLPGCGDPRKPLRGFWVTGDNNTSYSRWARLDLNGAPLCPVAV 122
 Db 82 ---PRLWIGLQPLPGCGDPRKPLRGFWVTGDNNTSYSRWARLDLNGAPLCPVAV 138
 QY 123 SAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPCGAAAAA---YSITYTTF 179
 Db 139 SAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPCGAAAAA---YSITYTTF 198
 QY 180 ARGADFOALPVGSSAAVAPLGLQMLCTAPPAVQGHWAAREAPGAWDCSVENGCGEHCACN 239
 Db 199 GARGADFOALPVGSSAAVAPLGLQMLCTAPPAVQGHWAAREAPGAWDCSVENGCGEHCACN 258
 QY 240 AIPGAPRCQCPAGALQADGRSCATASQSCNDLCEHFCVNPDPQSGYSQCMCTGYRLA 299
 Db 259 ASAGAPRCQCPAGALQADGRSCATASQSCNDLCEHFCVNPDPQSGYSQCMCTGYRLA 318
 QY 300 ADQHRCEVDVDCILBPSPCPQCVNTQGGFCHCYPNYDLVDGECVEPVDPCFRANCEYQ 359
 Db 319 ADGHRCEVDVDCILBPSPCPQCVNTQGGFCHCYPNYDLVDGECVEPVDPCFRANCEYQ 378
 QY 360 COPLNQTSLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECPGYILLDDGF 419
 Db 379 CLPLGQ-NYRCICAEAGFAPVDPDEPHRCQMFQNTACPADCDPNTQASCECPGYILLDDGF 437
 QY 420 ICTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARHIGTDC-----DSKVDGG-DS 472
 Db 438 LCADIDECN-GYCODECNLPGSYECICGPDSSALARHIGTDC-----DSKVDGG-DS 494
 QY 473 GSGEPPPSPTPGST-LTPPAVGLVHSG 498
 Db 495 GSGEPPPSPTPGST-LTPPAVGLVHSG 521
 RESULT 4.
 Q35370
 ID O35370 PRELIMINARY; PRT; 577 AA.
 AC O35370
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thrombomodulin.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;
 RP [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
 RA Wang J., Yao A., Wang J.Y., Hardin J.W., Hauer-Jensen M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Yao A., Wang J., Hardin J.W., Hauer-Jensen M.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF022743; AAB80760.1; -
 DR EMBL: AF022742; AAB80923.1; -
 DR HSP: P07204; IFGD.
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 0005529; F:calcium ion binding; IEA.
 DR GO: 0005529; F:sugar binding; IEA.
 DR GO: 0004888; F:transmembrane receptor activity; IEA.
 DR GO: 0007596; P: blood coagulation; IEA.
 DR InterPro: IPR000152; Asx hydroxyl_S.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR001491; Thrombomodulin.
 DR Pfam: PF00008; EGF; 3.
 DR Pfam: PF00059; Lectin_C; 1.
 DR PRINTS: PR00907; THROMBOMODULN.
 DR SMART: SM00034; CLECT. 1.
 DR SMART: SM00179; EGF_Ca; 2.
 DR PROSITE: PS00010; ASX HYDROXYL; 2.
 DR PROSITE: PS00041; C TYPE LECTIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_Ca; 2.
 KW EGF-like domain.
 SQ SEQUENCE 577 AA; 61844 MW; 0BE764C8BF18555F CRC64;
 Query Match 63.3%; Score 1790; DB 11; Length 577;
 Best Local Similarity 63.9%; Pred. No. 6.8e-140;
 Matches 321; Conservative 48; Mismatches 127; Indels 6; Gaps 5;
 QY 1 APAEPQPGSQCVHDCFPATFLNASQICDGLRGLMTVRSSVAADVVISLLNGD 60
 Db 19 ALAKLQPKGSCQVNECFALFQDPVTFDASQORLQHLMTVRSSVAADVVISLLS-D 77
 QY 61 GVGRRRLWIGLQPLPGCGDPRKPLRGFWVTGDNNTSYSRWARLDLNGAPLCPV 120
 Db 78 SMSDRP-WIGLQPLPGCGDPRKPLRGFWVTGDNNTSYSRWARLDLNGAPLCPV 136
 QY 121 AVSAAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEP-GAAAAVSYTYTTF 179
 Db 137 TVSTATEAAGEPAWEKPCENETKGFCEFFFAAFCEPLRVNTRDPEGAHISSTYNTPL 196
 QY 180 AARGADFOALPVGSSAAVAPLGLQMLCTAPPAVQGHWAAREAPGAWDCSVENGCGEHCACN 239
 Db 197 GVGADFOALPVGSSAAVAPLGLQMLCTAPPAVQGHWAAREAPGAWDCSVENGCGEHCACN 256
 QY 240 AIPGAPRCQCPAGALQADGRSCATASQSCNDLCEHFCVNPDPQSGYSQCMCTGYRLA 299
 Db 257 RSANGPRCVCPGSGDLQADGRSCATASQSCNDLCEHFCVNPDPQSGYSQCMCTGYRLA 316
 QY 300 ADQHRCEVDVDCILBPSPCPQCVNTQGGFCHCYPNYDLVDGECVEPVDPCFRANCEYQ 359
 Db 317 ADGHRCEVDVDCILBPSPCPQCVNTQGGFCHCYPNYDLVDGECVEPVDPCFRANCEYQ 376
 QY 360 COPLNQTSLVCVCAEGFAPIPHEPHRCQMFQNTACPADCDPNTQASCECPGYILLDDGF 419
 Db 377 QPWNSTHYNCICAEAGFAPVDPDEPHRCQMFQNTACPADCDPNTQASCECPGYILLDDGF 436
 QY 420 ICTDIDECENGFCGSGVCHNLPGTFECICGPDSSALARHIGTDCSGKY--DGGDSGSGEP 477
 Db 437 ICTDIDECNGQCECLTNECNLPGSYECICGPDSSALARHIGTDCSGKY--DGGDSGSGEP 496
 QY 478 PPS-PTFGSTLTTPPAVGLVHSG 498

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Db 497 PSNPTVSSSTVPPSGARPMHSG 518
RESULT 5
QB8JB5
ID QB8JB5 PRELIMINARY; PRT; 491 AA.
AC QB8JB5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Thrombomodulin precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
EX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK089479; BAC40898.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00059; Lectin_G; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00179; EGF_Ca; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_Ca; 2.
FT NON TER 491
SQ SEQUENCE 491 AA; 52904 MW; AE2007EEC68AD20D CRC64;

Query Match 62.9%; Score 1780.5; DB 11; Length 491;
Best Local Similarity 67.3%; Pred. No. 3.5e-139;
Matches 313; Conservative 43; Mismatches 104; Indels 5; Gaps 3;

QY 1 APAEPOGSGQVHEHDCFALPGPATFELNASQICDGLRHLMVTRSVAAVLSLLNGD 60
Db 19 ALAKLPTGSGQVHEHDCFALPGPATFELNASQICDGLRHLMVTRSVAAVLSLLNGD 60
QY 61 G-GVRRRLWIGLQPPGGDPRKLGFLRGFQWVTGDNNTSYSRWRLDNGAPLCPGLC 119
Db 79 SMDLGP---WIGLQPPGGDPRKLGFLRGFQWVTGDNNTSYSRWRLDNGAPLCPGLC 119
QY 120 VAUSAATVPSEPIWEQCEVKADGFLCEHPFATCRPLAVEP-GAAAAVSIYGTTP 178
Db 136 VTVSTATEAAGEPAWEKPCETETQGLCFEYFTASCRPLTWTNTRDPAAHISSTYNTP 195
QY 179 FAARGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSVGCEHAC 238
Db 196 FGVSAGDFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSVGCEHAC 238
QY 239 NAIPGAPCOCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGSGSCMCTGYQL 298
Db 256 NRSTNEPRCLCDPRMDLQADGRSCTASATQSCNDLCEHFCVNPDPGSGSCMCTGYQL 298
QY 299 ADQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNPNYDLVDGECVPEVDPFCFRANCEY 358
Db 316 AADGHRCEVDVDCILEPSPQRCVNTQGGFCHYCNPNYDLVDGECVPEVDPFCFRANCEY 358
QY 316 AADGHRCEVDVDCILEPSPQRCVNTQGGFCHYCNPNYDLVDGECVPEVDPFCFRANCEY 358

Query Match 49.5%; Score 1400.5; DB 11; Length 461;
Best Local Similarity 62.7%; Pred. No. 9.6e-108;
Matches 245; Conservative 37; Mismatches 104; Indels 5; Gaps 4;

QY 113 PLGCLPVAVSAAEATVPSEPIWEQCEVKADGFLCEHPFATCRPLAVEP-GAAAAA 170
Db 12 PLGCLPVAVSAAEATVPSEPIWEQCEVKADGFLCEHPFATCRPLAVEP-GAAAAA 170
QY 171 VSIYGTTPAARGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSV 230
Db 72 ISSTYNTPLGVSGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHWAREAPGAWDCSV 230
QY 231 NGGCEHACVNTAPGAPCOCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGSGSYSC 290
Db 132 NGGCEHACVNTAPGAPCOCPAGALQADGRSCTASATQSCNDLCEHFCVNPDPGSGSYSC 290
QY 291 MCETGYRLAADQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNPNYDLVDGECVPEVDP 350
Db 192 MCETGYRLAADQHRCEVDVDCILEPSPQRCVNTQGGFCHYCNPNYDLVDGECVPEVDP 350
QY 351 CFRANCEYQCCOPLNQTSYLCVCAEGFAPIPHEPHRCMFCNQATACPADCDENTQASCECP 410
Db 252 CFRANCEYQCCOPLNQTSYLCVCAEGFAPIPHEPHRCMFCNQATACPADCDENTQASCECP 410
QY 411 EGYTLDGDFICTDIDECENGSGFCVCHNLPGTGFECTCGPDSALARHIGTDCDSGKV--D 468
Db 411 EGYTLDGDFICTDIDECENGSGFCVCHNLPGTGFECTCGPDSALARHIGTDCDSGKV--D 468

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Db 312 EGFILDRSGSICDIDECGSECLTNECRNLPGSYECICGPTALAGQISKDCDPIPVLED 371
QY 469 GDSGSGSGPPPS-PTPGSTLTTPPAVLVHSG 498
Db 372 SEDGSGSGEPSSNPTVSVTPPSARMHSG 402

RESULT 7
Q81XK1
ID Q81XK1 PRELIMINARY; PRT; 652 AA.
AC Q81XK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Clq receptor protein precursor.
GN CD93.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] _SEQUENCE FROM N.A.
RA Steinberger P., Stoeckl J., Wille S., Szekeres A., Prager E.,
RA Staffler G., Kuenig S., Kohl P., Majdic O., Knapp W., Stockinger H.;
RT "Identification of CD93 as the Clq receptor protein (ClqR) by
RT retroviral expression cloning.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295142; CAC82720.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; ASX_HYDROXYL; IEA.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00108; Tissue_fac; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 5.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 652 Clq RECEPTOR PROTEIN.
SQ SEQUENCE 652 AA; 69521 MW; 97549BA62CAF225E CRC64;

Query Match
Best Local Similarity 31.6%; Score 578; DB 4; Length 652;
Matches 175; Conservative 52; Mismatches 39; Indels 126; Gaps 31;

QY 6 QPGSGS-----CVHEHDFCALYPGPATFLNASQICDGLRGLHMTVRSVAAD-----VI 53
Db 17 QPGAGTGADTEAVVCGVTACTYTAHSGKLSAAEAQNHCNQNGNGLAVKSEEAQHVRVL 76
QY 54 SLLINGDGVGR-RLWTGLQLPPG-CGDPRKGLRPGFWVTGDNNTSYRWARLDLN 110
Db 77 AQLLRREALTARMSKFWTGLQREKCKLDPSL--PLKGFVWVGGEDTFYSNWHKELRN 134
QY 111 GAPLCGLPLCA--VSAEAATVPE--PINEEQCC-----EVKADGFLCFHFHPATCRPLA 161
Db 135 SC--ISKRCVSLLDLSQLPLSRPLKWSGEFGCGSPGSGNIEGFVCKFSFGKRCRPLA 192
QY 162 V-EPGAAAANVITYGTPTFAARGADFOALPVGSSAAVAPLGLQLMC-TAPPGAQVQHW-- 217
Db 193 LGPG-----QVTVTPPTTSSSLEAVFPASAANVA-----CGEGDKDQTSQHYFL 239

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QY 218 -AREAFGAMD-----CSVENGGEHAC-NAIPGAPRCOCPAALQADGRS 261
Db 240 CREKADVEDWGSSGFLCVSPKYGKFNNGGCHQDCFEFGDGSFLCGCRPFRLLDLVT 299
QY 262 CTASATQSCNDLCE--HFCVNPDPQGSYSYSCMCETGYRLAADQHRCEDVDDCILEPSPCP 319
Db 300 C-ASRNPCSSPCRGATCALGP-HGKNYTCRCPQGYQLDSSQLDCVDVDEC--QSPCA 355
QY 320 QRCVNTGGFECHECVENYDLVDEGCEVFPVDFRANCEYQCQPLNQTSLYLCVCAEGFAP 379
Db 356 QECVNTGPGFRCECWGY-----EPGGP-----GEGACQDVDE-----CALGRSP- 395
QY 380 PHEPHRCQMFNCQTACPADCDPNTQAS--CECEGYIL--DDGFICTDIDEC--ENGGPC 433
Db 396 -----CAQGC-TNTDGSFHCSEGYVLAGEGTQCQDQVDECVGFGPLC 439
QY 434 SGVCHNLPGTPECICGPDASALAHIGTDCDQSKV-----DGGDSGSGE-----P 477
Db 440 DSLCFNTQGSFHCGLPGWVLAPN-GVSCTMGPVSLGPPSGPPDEEDKGEKGSVTPRAA 498
QY 478 PPSPTPGSTLTTPPA 491
Db 499 TASPTRGEGTPKA 512

RESULT 8
Q9HCUO
ID Q9HCUO PRELIMINARY; PRT; 757 AA.
AC Q9HCUO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor endothelial marker 1 precursor (Endosialin protein).
GN TM1 OR ENDOSIALIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] _SEQUENCE FROM N.A.
RP MEDLINE=20407466; PubMed=10947988;
RX St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
RN [2] _SEQUENCE FROM N.A.
RX MEDLINE=21269274; PubMed=11084048;
RA Christian S., Ahorn H., Koehler A., Eisenhaber F., Rodi H.P.,
RA Garin-Chesa P., Park J.E., Rettig W.J., Lenter M.C.;
RT "Molecular cloning and characterization of Endosialin, a C-type
RT lectin-like cell surface receptor of tumor Endothelium.";
RL J. Biol. Chem. 276:7408-7414(2001).
DR EMBL; AF275142; AAG00867.1; -.
DR EMBL; AJ295846; CAC34381.1; -.
DR HSSP; P07204; 1ZAQ.
DR Genew; HGNC:18219; CD164L1.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR InterPro; IPR000152; ASX_HYDROXYL_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain; Signal.

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FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 757 TUMOR ENDOTHELIAL MARKER 1.
SQ SEQUENCE 757 AA; 80858 MW; C96363EALFD9FFA0 CRC64;

Query Match 20.4%; Score 578; DB 4; Length 757;
Best Local Similarity 33.6%; Pred. No. 2.2e-39;
Matches 170; Conservative 41; Mismatches 181; Indels 114; Gaps 23;

QY 3 AEPQGGQCVHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLINGDG 62
DQ 23 AEPQGGQCVHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLINGDG 62
DQ 23 AEPQGGQCVHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLINGDG 62
QY 63 VGRRLWTGLQPGCGDKPLRGLRQWVTGNNTSYSRWARLDNGAPLGLCVAV 122
DQ 78 PASRLWTGLQPGCGDKPLRGLRQWVTGNNTSYSRWARLDNGAPLGLCVAV 122
DQ 78 PASRLWTGLQPGCGDKPLRGLRQWVTGNNTSYSRWARLDNGAPLGLCVAV 122
QY 123 SAABATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYTTPFAAR 182
DQ 135 EAS-----GEHWLEGSTLAVDGLYLCQFEGACPALQDAGQAGPAV---YTTTFFLV 186
DQ 135 EAS-----GEHWLEGSTLAVDGLYLCQFEGACPALQDAGQAGPAV---YTTTFFLV 186
QY 183 GADFOALPVGSSAAV---APLGLQLMCTAPGAVQGHWAREAP---GAWDCSVENGCGEH 236
DQ 187 STEFEMLPFGSVAAVQCAQAGRSLLCVKQPEGVG-WSRAGPLCLGT-GCSPDNGCGEH 244
DQ 187 STEFEMLPFGSVAAVQCAQAGRSLLCVKQPEGVG-WSRAGPLCLGT-GCSPDNGCGEH 244
QY 237 AC-NAIPGAPRCQCPAGAAQADGRSCTASATQS-CNDLCEHFCVNPDPGYSYSCMCET 294
DQ 245 ECVEVDGHSRCCTEGFRLAADRSCEDPCAAPCEQCE-----PGPGQGYSCHCRL 298
DQ 245 ECVEVDGHSRCCTEGFRLAADRSCEDPCAAPCEQCE-----PGPGQGYSCHCRL 298
QY 295 GYRLAADQ-HRCEVDVDCILEPSPCPORCVNTGGRECHVYNDLVGSCVPEVPCFR 353
DQ 299 GFRPAEDDPRHRCVDTDECQI-AGVQCMQVNYGGFECYCSGHELE----- 344
DQ 299 GFRPAEDDPRHRCVDTDECQI-AGVQCMQVNYGGFECYCSGHELE----- 344
QY 354 ANCEYQCOPLNQTSLYLCVCAEGFAPIPHEPHRCQMFNCTACPADCDP-----NTQASCEC 409
DQ 345 -----ADGIS----- 345
DQ 345 -----ADGIS----- 345
QY 410 PEGVILDDGFICTIDIDE---CENGFGSGVCHNLPGT---PECICGDSALARIHGTDCDS 464
DQ 365 GD-ELLDDGDEDEDEAWKAFNGWT-----EMPGILMWEPTQPDFFALAYRSPED- 417
DQ 365 GD-ELLDDGDEDEDEAWKAFNGWT-----EMPGILMWEPTQPDFFALAYRSPED- 417
QY 465 GKVDGDSGSGEPPTGPTGSLTTPP 490
DQ 418 -----REFQIPYPTWPPP 432
DQ 418 -----REFQIPYPTWPPP 432

RESULT 9
Q91ZV1
ID Q91ZV1 PRELIMINARY; PRT; 765 AA.
AC Q91ZV1;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Endosomal.
GN TEM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Thymus;
RA MEDLINE=21486432; PubMed=11489895;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Gilbert D.J., Jenkins N.A., Bies J., Garfield S., Pastorekova S.,
RA Oue A., Wolff L.;
RT "Molecular Characterization of the Mouse Tem1/endosomal Gene
RT Regulated by Cell Density in Vitro and Expressed in Normal Tissues in
RT Vivo."
RL J. Biol. Chem. 276:38795-38807(2001).
DR EMBL; AF388572; AAK84664.1;
DR MGD; MGI:1917695; Tem1.
DR GO; GO:0005737; Cytoplasm; IDA.
DR InterPro; IPR000152; Asx_hydroxyl_S.

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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF0000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00041; C_TYPE_LCTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 765 AA; 81823 MW; 07B3225E5DD13A03 CRC64;

Query Match 20.0%; Score 566.5; DB 11; Length 765;
Best Local Similarity 38.9%; Pred. No. 2e-38;
Matches 139; Conservative 37; Mismatches 146; Indels 35; Gaps 16;

QY 2 PAPQGGQCVHDCFALYPGPATFLNASQICDGLRGLHMTVRSSVAADVISLLINGDG 61
DQ 20 PWTPEPRAA-CGPPSCYALFPRRTTFLAWRACRELGNLATPTPEERQVDSLV--- 74
DQ 20 PWTPEPRAA-CGPPSCYALFPRRTTFLAWRACRELGNLATPTPEERQVDSLV--- 74
QY 62 GVGRRR--LWIGLQLPGGGDKPLRGLRQWVTGNNTSYSRWARLDNGAPLGLCV 119
DQ 75 GVGFANGLLWIGLQARQCCQQR--PLRGFTWTTGDTQDTAFNTWAQPALEG-PCAQRC 131
DQ 75 GVGFANGLLWIGLQARQCCQQR--PLRGFTWTTGDTQDTAFNTWAQPALEG-PCAQRC 131
QY 120 VAVSAEATVPSEPIWEEQCEVKADGFLCEHFPATCRPLAVEPGAAAVSITYTTPF 179
DQ 132 AALEAS-----GEHWLEGSTLAVDGLYLCQFEGACPALQDAGQAGPAV---YTTTFF 183
DQ 132 AALEAS-----GEHWLEGSTLAVDGLYLCQFEGACPALQDAGQAGPAV---YTTTFF 183
QY 180 ARGADFOALPVGSSAAV---APLGLQLMCTAPGAVQGHWAREAP---GAWDCSVENGCG 234
DQ 184 NLVSSEFELPFGSVAAVQCAQAGRSLLCVKQPEGVG-WSQTPGLCPTGCGPDNGCG 242
DQ 184 NLVSSEFELPFGSVAAVQCAQAGRSLLCVKQPEGVG-WSQTPGLCPTGCGPDNGCG 242
QY 235 EHAC-NAIPGAPRCQCPAGAAQADGRSCTASATQS-CNDLCEHFCVNPDPGYSYSCMC 292
DQ 243 EHECEVDGHSRCCTEGFRLAADRSCEDPCAAPCEQCE-----PGPGQGYSCHC 296
DQ 243 EHECEVDGHSRCCTEGFRLAADRSCEDPCAAPCEQCE-----PGPGQGYSCHC 296
QY 293 ETGYRLAADQ-HRCEVDVDCILEPSPCPORCVNTGGRECHVYNDLVGSCVPEV 347
DQ 297 RLGFPAEDDPRHRCVDTDECQI-AGVQCMQVNYGGFECYCSGHELEADGISCP 352
DQ 297 RLGFPAEDDPRHRCVDTDECQI-AGVQCMQVNYGGFECYCSGHELEADGISCP 352

RESULT 10
Q91V98
ID Q91V98 PRELIMINARY; PRT; 765 AA.
AC Q91V98;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor endothelial marker 1 precursor (Endosomal).
GN TEM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RA "Cell surface tumor endothelial markers are conserved in mice and
RA humans."
RT Cancer Res. 61:6649-6655(2001).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129S6/SvEvTac; TISSUE=Spleen;
RA MEDLINE=21486432; PubMed=11489895;
RA Opavsky R., Haviernik P., Jurkovicova D., Garin M.T., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Bies J., Garfield S., Pastorekova S.,
RA Oue A., Wolff L.;

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"Molecular Characterization of the Mouse Tem1/endosomal Gene Regulated by Cell Density in Vitro and Expressed in Normal Tissues in Vivo.";

J. Biol. Chem. 276:38795-38807(2001).

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Buetow C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F., Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hsieh L., Brownstein M.J., Ustin T.B., Toehiyuki S., Casavant T.L., Scheetz T.E., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Richards S., Worley K.C., Hale S., Garcia J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP	SEQUENCE FROM N.A.
RC	TISSUE=Olfactory epithelium;
RA	Strausberg R.;
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBDJ databases.
DR	ENBL; AF378758; AAL11995.1; -
DR	ENBL; AF388573; AAK84655.1; -
DR	ENBL; BC048318; AAH46318.1; -
DR	MGD; MGI:1917695; Tem1.
DR	GO; GO:0005737; C.cytoplasm; IDA.
DR	InterPro; IPR000152; Asx hydroxyl_s.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR001304; Lectin C.
DR	InterPro; IPR000436; Sushi_SCR_CCP.
DR	Pfam; PF00008; EGF; 2.
DR	Pfam; PF00059; lectin_c; 1.
DR	Pfam; PF00084; sushi_1.
DR	SMART; SM00034; CLECT; 1.
DR	SMART; SM00179; EGF_CA; 1.
DR	PROSITE; PS00010; ASX HYDROXYL; 1.
DR	PROSITE; PS00041; C TYPE LECTIN_2; 1.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS01187; EGF_CA; 1.
KW	EGF-like domain; Signal.
FT	SIGNAL 1 17
FT	CHAIN 18 765
SQ	SEQUENCE 765 AA: 81813 MW: 572066CCGCGCCTGGAGCA
	TUMOR ENDOTHELIAL MARKER 1.

Query Match	20.0%;	Score 566.5;	DB 11;	Length 765;
Best Local Similarity	38.9%;	Pred. No. 2e-38;		
Matches 139; Conservative	37;	Mismatches 146;	Indels 35;	Gaps 16;

QY	2	PAEPOFGSQCVHDCFALVPGPATFINASQICDGLRGHLMTVRSSVAADVISLLNGDG	61
Db	:	: : : : : :	:
	20	PWTPEPRAA-CGPSSCYALFFRRRTTLEAWRACRELGGNLATPTPEAQRVDSLV----	74
QY	62	GVGRRR--LWIGLQLPPGCGDKRLGRGFOWVTGDNTTSYSRWARLDLNGAPLCGPLC	119
Db	:	: : : : : :	:
	75	GVGPANGLLWIGLQRARQCQPOR--PLRGFIWTTGDQDTAFTNWAQPAPEG-PCPAQRC	131
QY	120	VAVSAAEAATVPSEPIWEIEQQCEVKADGFLCEHFHPATCRPLAVEPGAAAAAVITGTTP	179
Db	:	: : : : : :	:
	132	AALAEAS-----GEHRWLGSCTIANDGYILCOQFGFEGCAPLPLEVGAQPAV---YTTPF	183

QY	180	AARGADFOALPVGSSAAV---	APLGLQLMCTAPPAGAVQGHWAREAP--	CAWDCSVENGGC	234
		:::	:::	:::	
Db	184	NLVSEFEFWLPGSVAAVQCCAGRCASLLCVKQPSGGVG-	WSQTGPLCBGTGCGPDNGCC	242	
		:::	:::	:::	
QY	235	EHAC-NATPGAPRCOCAPAGALQADGRSCTASATQS-	CNDLCEHFCVPNFPDOPGVSQWC	292	
		:::	:::	:::	
Db	243	EHECVEEDGAVSCRSBGRFLADGHSCDEPCACAPCEQQE-	-----PGGPGQYSCHC	296	
		:::	:::	:::	
QY	293	ETGYRLANDQ-HRCHDVDDCILPSPQRCQVNTGGFEC	HCYPNYDL-VDGECVEP	347	
		:::	:::	:::	
Db	297	RLGFRPAEDDPHRCVDTDECOI-AGVCQCMCVNYVGGFEC	YCSBEGHEADGISCP	352	
		:::	:::	:::	
RESULT 11					
QSTVQ2					
ID	Q9TVQ2	PRELIMINARY;		PRT;	1664 AA.
AC	Q9TVQ2;				
DT	01-MAY-2000	(TReMBLrel. 13, Created)			
DT	01-MAY-2000	(TReMBLrel. 13, Last sequence update)			
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)			
DE	Y64G10A.7	protein.			
GN	Y64G10A.7				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
OC	Rhabditidae; Pelodierinae; Caenorhabditis.				
OX	NCBI TaxID=6239;				

[1] SEQUENCE FROM N.A.
RA Mortimore B.J.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[2] SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
[3] SEQUENCE FROM N.A.
RA Ainscough R.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117206; CAB60454.1; -
DR EMBL; AL110498; CAB60454.1; JOINED.
DR EMBL; AL110498; CAB57911.1; -
DR EMBL; AL117206; CAB57911.1; JOINED.
DR HSP; P00736; IAPQ.
DR WormPep; Y64G10.7; CE24549.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00008; EGF; 22.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SMC0179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 22.
DR PROSITE; PS01186; EGF_2; 24.
DR PROSITE; PS01187; EGF_CA; 3.
DR EGF-like domain.
KW 1654.AA. 170270.MV

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Query Match      15.2%; Score 431; DB 5; Length 1664;
Best Local Similarity 29.7%; Pred. No. 8e-27;
Matches 126; Conservative 40; Mismatches 178; Indels 80; Gaps 19;

QY 101 YSRWRLDLNGALPLGCLCAVSAAE-----ATVPSEPIWEEQOCE--VKADGFTCEP 151
      ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 YLRFARFRRGCSKCLLEVAQNCSDALCHNGGTCVPSEHNDNEQCECPVGTGAKCQY 115
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 HFPATCRPLAVPEGMAAAAVSTIYTFPAARGADFOALPVGSSAAVAPLGLQMLCTAPPG 211
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 116 D-ANEC--MANNOCCEHCVN-TIGTTY-----CRCWPG 145
QY 212 AVQHWAREAPGDCVSENGGCEHACNAIPGAPRCOCAGALOADGRSCTA-----264
Db 146 FELSGDNTCSDDICAVSNGGSDRCVNSPGGFRCDPDSLDLHADGRTGSGFHENL 205
QY 265 ---SATQSC---NDLCEHFCVNPDPQSGYSKCMCTGYRLAADQHRCEVDVDDCILEPSPC 318
Db 206 ILIKVTSCTSDNGGCEHEC-ENDSNGEFYRCRCRVGFKLSKNRSCQVDFCFDNKGGC 264
QY 319 PRCVNTQGGFECHCVNYDL-VGECVEVPDPCFRAN-CEYOCQPLNQTSLYLCVCAEFG 376
Db 265 QHCTNNHGAQCCQYFGHLSYDRSCVDIDECANNGCEHFCENVKGT-YACKCREGY 323
QY 377 APIPEPHRCOMP-----CNQATCAPADC--DPNTQASCECEPGYIL-DDGFICTDIDEC- 427
Db 324 -QLGRDRTCEEMLGCGVNGGCGQCHDCYDQPGGHVCKRCRNYILLANDQKLCHECH 382
QY 428 ENGFGSCGVCHNLPGHFEICIGPDSALAHIGT-----DKVDCGDSG 473
Db 383 ENNGDCSQICVNLAGSVEQCKPGLMKDRKTCEDISECSNNGGCEQICSNQEGGYMC 442
QY 474 SGEP 477
Db 443 SCEP 446

RESULT 12
ID 088281 PRELIMINARY; PRT; 1574 AA.
AC C08281;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE MEGF6.
GN MEGF6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=98360089; PubMed=983030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple EGF-
RL like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL; AB011532; BAA32462.1; -.
DR PIR; T13954; T13954.
DR HSP; P00736; 1APO.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00008; EGF; 20.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; 23.
DR PROSITE; PS01186; EGF_2; 23.
DR PROSITE; PS01187; EGF_CA; 5.
DR KW EGF-like domain.
SQ SEQUENCE 1574 AA; 165445 MW; 2B48533D8F7F6E7 CRC64;

Query Match
Best Local Similarity 34.1%; DB 11; Length 1574;
Matches 104; Conservative 28; Mismatches 101; Indels 72; Gaps 17;

QY 206 CTAPPG-AVOGHWAREAPGDCVSENGGCEHACNAIPGAPRCOCAGALOADGRSCTA 264
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

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Db 147 CRCPGYQIQGD-GKTCQDVDECRANHGQHRVNTPGSYLCECKPGFRLHTDGRCTL- 204
QY 265 SATQSC---NDLCEHFCVP-----NPDQPGSYSCM-----291
Db 205 -AISCTLNGGCGHQCQVLTQHRCCQCPQYQLEDGRRCVRRSPCAEANGGCMHICQ 263
QY 292 -----CETGYRLAADQHRCEVDVDDCILEPSPCQRCVNTQGGFECHCVNYDL-VD 341
Db 264 EURLGAHOCCHFGYQLAADRKTCEDVDICALGLAQCAHGLCLNTQGSFKVCVCHAGYELGAD 323
QY 342 G-EC-----VEPYDPCFRAN-CEYOCQPLNQTSLYLCVCAEFGAPIPHEPHRCOMFC-----390
Db 324 GRQCVRIMEIIVNSCEANGGCGSHGSH-TSTGPLCTCPRGY-----ELDEQKTCIDID 377
QY 391 ---NOTACPADCDPNTQA--SCECEGYILD-DGFICTDIDECENG-GFSCGVCHNLPGT 443
Db 378 DCANSFCCQAC-ANTPGYEGSCFAGYRLNTDGGCEDVDCEASGHGCEHCNLAGS 436
QY 444 FECIC 448
Db 437 FOCFC 441

RESULT 13
QYVS89
ID QYVS89 PRELIMINARY; PRT; 1409 AA.
AC QYVS89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE CG7526 protein.
GN CG7526.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Bonzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Numoo J.,
 RA Paclob J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoenunavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003558; AAF50538.2;
 DR HSSP; P00736; IAP0.
 DR FlyBase; F8gn0035798; CG7526.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; R:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR InterPro; IPR000152; Asx hydroxylase; IEA.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR003410; HVALin.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF; 11.
 DR Pfam; PF00084; sushi; 2.
 DR PRINTS; PR00907; THROMBOMODULN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00181; EGF; 13.
 DR SMART; SM00179; EGF CA; 14.
 DR PROSITE; PS00010; ASX HYDROXYL; 8.
 DR PROSITE; PS01186; EGF 2; 9.
 DR PROSITE; PS01187; EGF CA; 10.
 DR EGF-like domain.
 SQ SEQUENCE 1409 AA; 154131 MW; F9A0DE1478AF354C CRC64;

Query Match 13.6%; Score 386; DB 5; Length 1409;
 Best Local Similarity 32.1%; Pred. No. 3.5e-23;
 Matches 99; Conservative 33; Mismatches 110; Indels 56; Gaps 18;

QY 206 CTAPPGAVQV-----HWAREPAGW-----DCSVNGGCEHACNAIPG 243

Db 563 CLCPFPYALGLDNHIVTSLNSSFITDSTSETPSAHTCLDIDECSLANGNSHFCQNEPG 622
 QY 244 APRCQCPAGALQADGRSCTASATOSC---NDLCEHFVCPNPDPQGSYSYCMCETGYRLAA 300
 Db 623 GFQACPLGLYALSEDWRTG--QDIDECDSNGQCSQLCL---NQFGGFACACETGFELTP 677
 QY 301 DQHRCEVDVDDCILERSPCQRCQVNTQGGFECHYNYDLVDGE--CVEPVDPC---FRAN 355
 Db 678 DQFGCADIDECSDYGNCSDDICINLLGTHACACERGYELAKDKLSCLD--VDECAGLGG 736
 QY 356 CEYQCOPLNOT--SYLCVCAEGFAPIPHEPHRCQMFNCQATACEA--DCDNTQASC----- 407
 Db 737 CSHEC--INAKTFEGGCPGLG--IINDDGR-----SCSPALVGCPPGTQRSADGAP 785
 QY 408 -RCPEGYLDDGFICTDIDEC--ENGCGSGVCHNLPGTFECICG--DSALARHI 458
 Db 786 IECNPGYTLGSDDKCVDIDECQKQNGG--CSHRCSNTEGSKCSPGYELDSQDKTCQDI 844
 QY 459 GTDCDSGK 466
 Db 845 -DECDQDK 851

RESULT 14

P87363 PRELIMINARY; PRT; 708 AA.
 AC P87363;
 DT 01-MAY-1997 (TREMELrel. 03, Created)
 DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Fibrillin-1 (Fragment).
 GN FBNI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20152896; PubMed=10691037;
 RA Zhou G., Price C.E., Rosenquist T.H., Gadson P.F., Godfrey M.;
 RT "Partial cloning and sequencing of chick fibrillin-1 cDNA.";
 RL In Vitro Cell. Dev. Biol. Anim. 36:19-25 (2000).
 DR EMBL; U88872; AA848531.1;
 DR HSSP; P07204; 2AD4.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx hydroxylase.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002212; Fibrin-assoc.
 DR Pfam; PF00008; EGF; 13.
 DR Pfam; PF00683; TB; 2.
 DR SMART; SM00179; EGF CA; 14.
 DR PROSITE; PS00010; ASX HYDROXYL; 13.
 DR PROSITE; PS01186; EGF 2; 10.
 DR PROSITE; PS01187; EGF CA; 13.
 DR EGF-like domain.
 KW NON TER 708
 FT SEQUENCE 708 AA; 76164 MW; C247271C1DF73361 CRC64;

Query Match 13.3%; Score 376; DB 13; Length 708;
 Best Local Similarity 31.8%; Pred. No. 1.1e-22;
 Matches 112; Conservative 26; Mismatches 108; Indels 106; Gaps 20;
 QY 226 DCSVNGGCEHACNAIPRCQCPAGALQADGRSCTASATOSCNDLCEHFVCPNP--- 282
 Db 223 ECSIMNGGCENFCGSGSEYSCSKQGFLMPDRTCT-----DDE--CEDNPNIC 272
 QY 283 -----DQPGSYSCMCTGYRLAADQHRCEVDVDDCILERSPC-FQRCVNTQGGFECHYCP 335
 Db 273 DGGQCTNIPGEYRCLCYDGFVASEDMKTCVDVNECDLHFNICLSGTCTKSGFICHDM 332

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QY 336 NYDLVDGE--CPEVDPC--FRANCEYQCQPLN-QTSYLCVCAEGFA-----PIP 380
Db 333 GYSKKGTTGCTD-INECEIGAHCNDRHAVCTNIPGSFKSCSSGWIENGKICTDLDECS 391
QY 381 HEPHRCQMFNCQTACPADCDPNTQAS--CECPGYILDDGFICTDIDE-----CENG- 430
Db 392 NGTHKCSPH-----ADC-KNTMGSYRCLCKEGY-TGDGFTCTDLDECSENLCENGQ 442
QY 431 -----GF-----CS-----GVCHNLPCTFECICGPDLSALA 455
Db 443 CLNAPGGYRCCEMDGFLPSLDGKACEDIDEGSLNLCVYGTCHNLPGLFRCECEVGYELD 502
QY 456 RHIG-----TDCDSK-VDGSDSGSEPPSPFTFGSTLTPPAVLV 495
Db 503 RSGGNCCTDVNECADPTTCISGTCVNTAGSYCECPD-----FELNPTRVGCV 550

RESULT 15
Q9WUH9
ID Q9WUH9 PRELIMINARY; PRT; 2906 AA.
AC Q9WUH9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibrillin-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99350231; PubMed=10419698;
RA Yang Q., Ota K., Tian Y., Kumar A., Wada J., Kashiwara N., Wallner E.,
RA Kanwar Y.S.;
RT "Cloning of rat fibrillin-2 cDNA and its role in branching
RT morphogenesis of embryonic lung.";
RL Dev. Biol. 212:229-242(1999).
DR EMBL; AF135060; AAD34439.1; -.
DR HSP; F3555; IEMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Aex_Hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 44.
DR Pfam; PF00583; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS01187; EGF_CA; 43.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 2906 AA; 313371 MW; 9EE64E727044EF58 CRC64;
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Query Match 13.3%; Score 375; DB 11; Length 2906;
Best Local Similarity 32.9%; Pred. No. 6.5e-22;
Matches 102; Conservative 24; Mismatches 92; Indels 92; Gaps 18;

QY 226 DCSVENGGCHACNAIPGAPROCPAGALQADGRSCTASATQSCNDLCEHFVCPNPD-- 283
Db 1237 ECMIMNGGCDTQCTNSRGSEYCSGYALMPDGRSCA-----DIDE--CENNPDI 1286
QY 284 -----QPGSYSCMETGYRLAADQRCEDVDCCILEPSPCP-ORCVNTQGGFECHCYP 335
Db 1287 DGGQCTNIPGEYRCLVDGFMASMDKMTICIDVNECDLNPNICMFGECENTKGSFICHQ 1346
QY 336 NYDLVDGE--CPEVDPC--FRANCEYQCQPLN-QTSYLCVCAEGFA-----PIP 380
Db 1347 GYSVKKGATGCTD-VDECEIGAHCNDRHAVCTNIPGSFKSCSSGWIENGKICTDLDECA 1405
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QY 381 HEPHRCQMFNCQTACPADCDPNTQAS--CECPGYILDDGFICTDIDE-----CENG- 430
Db 1406 NGTHQCSI-----NAQC-VNTPGSYRCACSEGF-TGDGFTCSVDDECAENINLCENGQ 1456
QY 431 -----GF-----CS-----GVCHNLPCTFECICGPDLSALA 455
Db 1457 CLNVPGAYRCECEMGFTPASDRSCQDIDECSTQNICVFGTCTNNLPGMFHCICDDGYGLD 1516
QY 456 RHIG--TDCC 463
Db 1517 RTGGHCTDID 1526
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Search completed: June 9, 2004, 08:50:01
Job time : 39.5 secs